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11435 bp mRNA linear PRI 31-JAN-1994	ntigen of monoclonal						Vertebrata; Euteleostomi;	!; Hominidae; Homo.			
bp mrna	type) for a						Craniata;	. Catarrhini			
HSMKI67A 11435	H.sapiens mki67a mRNA (short type) for antigen of monoclonal antibody Ki-67.	X65551 7 27 11555	X65551.1 GI:415820	antigen; monocional antibody.	HOMO Sapiens.	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 11435)	Gerdes Fors, J.	Direct Submission
HSMKI67A/c LOCUS	DEFINITION	N		ų.		ORGANISM			REFERENCE	SS	TITLE

JOURNAL

REFERENCE AUTHORS

TITLE

REMARK

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RTRVQKVQVKEEPSAVKFTQTSGETTDADKEPAGEDKGIKALKESAKQTPAPAASVTG
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KFTRTSGETTHTHREPAGDGKSIRTFKESPKQILDPAARVTGMKKWPRTPKEEAQSLE
DLAGFKELFQTPGPSEESMTDEKTTKIACKSPPPESVDTPTSTKQWPKRSLRKADVEE
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KAQALEDLAGFKELFQTPGHTEELVAAGKTTKIPCDSPQSDPVDTPTSTKQRPKRSIR
KADVEGELLACRNLMPSAGKAMHTPKPSVGEEKDIIIFVGTPVQKLDLTENLTGSKRR
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DILQMICSKRRSGASEANLIVAKSWADVVKLGAKQTQTKVIKHGPQRSMNKRQRRPAT
PKKPVGEVHSQFSTGHANSPCTIIIGKAHTEKVHVPARPYRVLNNFISNQKMDFKEDL
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RPFETYKENIELKENDEKMKAMKRSRTWGQKCAPMSDLTDLKSLPDTELMKDTARGQN
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KKILCKSPQSDPADTPTNTKQRPKRSLKKADVEEEFLAFRKLTPSAGKAMHTPKAAVG
EEKDINTFVGTPVEKLDLLGNLPGSKRRPQTPKEKAKALEDLAGFKELFQTPGHTEES
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TGSKRHPKTKEKAQPLEDLAGWKELFQTPVCTDKPTTHEKTTKIACRSQPDPVDTPTS
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DKNPASSKRRLKTSLGKVGVKEELLAVGKLTOTSGETTHTHTEPTGDGKSMKAFMESP
                 (bases 1 to 11435)
Schluter, C., Duchrow, M., Wohlenberg, C., Becker, M.H., Key, G., Flad, H.D. and Gerdes, J.
The cell proliferation-associated antigen of antibody Ki-67: a very large, ubfquitous nuclear protein with numerous repeated elements, Fepresenting a new kind of cell cycle-maintaining proteins 9403433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MWPTRRLVTIKRSGVDGPHFPLSLSTCLFGRGIECDIRIQLPVV
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FSAQNAAKQPSDKCSASPPLRRQCIRENGNVAKTPRNTYKMTSLETKTSDTETEPSKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPPNTPLKRGEAPTKRKSLVMHTPPVLKKIIKEOPOPSGKOESGSEIHVEVKAOSLVJ
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Submitted (11-APR-1992) J. Gerdes, Forschungsinstitut Borstel, Div
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db_xref="GI:415821"

db_xref="GI:415821"
                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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/cell_line="IM9"
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="lambda gtll"
1. .107
                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .11435
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/gene="mki-67"
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/gene="mki-67"
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KISRRYLRAPKVEPVGDVVSTRDPVKSQSKSNTSLPPLIPFKRGGGKDGSVTGTKRLRC
MPAPEEIVBELPASKKQRVAPRARGKSSEPVVIMKRSLRTSAKRIEDAEELUSNDMKT
WREHKLQDSVPENKGISLRSRRQDKTSAERQOITTEVFVLAERTEINRNEKFPMKTSPE
MDIQNPDDGARKPIPFRKFCLRSARQNESSQPKVAEESGGGKSAKVLMQNQKG
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RPRTRAOKVEVKEELLAVGKLTQTSGETTHTDKEPVGEGKGTKAFKQPAKRNVDAEDV
                           IGSRROPRAPKEKAOPLEDLASFOELSOTPGHTEELANGAADSFTSAPKOTPDSGKPL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 12493)
Deinnert,I., Boehle,A., Gerdes,J. and Flad,H.D.
Antisense oligonorleocides for treating proliferating cells
Patent: WO 9961607-A 1 02-DEC-1999;
DEINER IRNA (DE); BOEHLE ANDREAS (DE); GERDES JOHANNES (DE); FLAD
HANS DIETER (DE); FORSCHUNGSZENTRUM BORSTEL ZENT (DE)
Location/Qualifiers
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DITBULTGSKRRPQTPKEERAQALEDLTGFKELEVGTPGHTEBERAAAGKTTMPCESSPP
ESADTPTSTRRQPFRTELERAQALEDLTGFRELEVGTPGHTEBERAAAGKTTMPCESSPP
ESADTPTSTRRQPFRTELERNOVGELSALKKLTQTGGETTHTDKVGGEBCKSINAFRE
TAKOKLDPAASVTGSKRHPKTKERAQPLEDLAGWKELFQTPVCTDKPTTHEKTTKIAC
REQDPUPUTPTSSKPOGKRENKNYDFEEFFALKTRPSGERAHTTRFASTRIAC
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AKVACKSSQPDLDKNPASSKRRLKTSLGKVGVKEELLAVGKLTQTSGETTHTHEPTGT
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ASFPLYEPAKMKTPVQYSQQQNSPQKHKNKDLYTTGRRESVNLGKSEGFKAGDKTLTP
RKLSTRNRTPAKVEDAADSATKPENLSSKTRGSIPTDVEVLPTETEIHNEPFLTLMLT
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SKANKRQRPRAPTKKUPGRHSQFSTGHANSPCTIIIGKAHTEKVHVPARPYRVINNF
ISNOKMBFREDLSGIABEMFKTPVK KOPQLTGTCHIAISISBELLGKOPGGTDSGEEPL
LPTSESFGGNVFFSAQNAAKQPSDKCSASPPLRRQCIBENGNVAKTPRNYKMTSLET
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PKRSLRKADVEEEFLALRKLTPSAGKAMLTPKPAGGDEKDIKAFMGTPVQKLDLAGTL
PGSKRQLQTPKEKAQALEDLAGFKELFQTPGHTEELVAAGKTTKIPCDSPQSDPVDTP
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MTNEKTTKVSYRASQPDLVDTPTSSKPQPKRSLRKADTEEEFLAFRKQTPSAGKAMHT
PKPAVGEEKDINTFLGTPVQKLDQPGNLPGSNRRLQTRKEKAQALEELTGFRELFQTP
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GRAMITPKAAVGEEKDINTPVGTPVBKLDLCAULGSKRRAPORPKEKKALEDLAGFK
ELFOTPGHTEESMIDDKITEVGTKSPOPDPVKTPTSKORLKISLGKVGVKEEVLPVG
KLTQTSGKTTQTHRETAGDGKSIKAFKESAKQMLDPANYGTGMERWPRTPKEEAQSLE
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KEKAQALEDLAGFKELFQTPGTDKPTTDEKTTKIACKSPQPDPVDTPASTKQRPKRNL
RKADVEEEFLALRKRTPSAGKAMDTPKPAVSDEKNINTFVETPVQKLDLLGNLPGSKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKQHCKVETHEQEAILHNFSSTNPTQVNGSVIDEPVRLKHGDVITIIDRSFRYENESL
QNGRKSTEFPRKIREQEPARRVSRSSFSSDPDEKAQDSKAYSKITEGKVSGNPQVHIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSVPTTQCLDNSKKNESPFWKLYESVKKELDVKSQKENVLQYCRKSGLQTDYATEKES
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GGHLRPELFDENLPPNTPLKRGEAPTKRKSLVMHTPPVLKKIIKEQPQPSGKQESGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTSDTETEPSKTVSTVNRSGRSTEFRNIQKLPVESKSEETNTEIVECILKRGQKATLL
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KVGVKEELLAVGKFTRTSGETTHTHREPAGDGKSIRTFKESPKQILDPAARVTGMKKW
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LEDLAGLKELFQTPVCTDKPTTHEKTTKIACRSPQPDPVGTPTIFKPQSKRSLRKADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLKIPLVKVDMKEEPLAVSKLTRTSGETTQTHTEPTGDSKSIKAFKESPKQILDPAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVKEDSTADDSKDSVAQGTTNVHSSEHAGRNGRNAADPISGDFKEISSVKLVSRYGEL
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/note="unnamed protein product"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Chases 1 to 12515)
Schluter, C., Duchrow, M., Wohlenberg, C., Becker, M.H., Key, G., Flad, H.D. and Gerdes, J.
The cell proliferation-associated antigen of antibody Ki-67: a very large, ubiquitous nuclear protein with numerous repeated elements, representing a new kind of cell cycle-maintaining proteins 7. Cell Biol. 123 (3), 513-522 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                 Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
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                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                               Length 12493;
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Sequence 7459 from Patent W00194629.
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/db_xref="taxon:9606"
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Pred. No. (
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Homo sapiens.
Homo sapiens
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FEATURES

exon gene CDS

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H.Sapiens DNA for Ki-67 antigen 5'-region (exon 1 6 2).
X94762
X94762.1 GI:1944550
Ki-67 gene; monoclonal antibody.
Homo sapiens.
Homo sapiens
PAEELNSNDMKTNKEEHKLODSVPENKGISLRSRRODKTEAEQOITEVFVLAERIEIN
RNEKKPMKTSPEMDIONPDDGARKPIPRDKVTENKRCLRSARONESSOPKVAEESGGG
KSAKVLMONQKGKGEAGNSDSMCLRSRKTKSOPAASTLESKSVQRVTRSVKRCAENPK
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/gene="mki67"
/note="partialy excluded by splicing"
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/gene="mki67"
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/number=15
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/gene="mki67"
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/gene="mki67"
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/gene="mki67"
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/gene="mki67"
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/gene="mki67"
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/gene="mk167
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ESADTPTSTRRQPKTPLEKRDVQKELSALKKLTQTSGETTHTDKVPGGEDKSINAFRE
TAKQKLDPAASVTGSKRHPKTKEKAQPLEDLAGWKELFQTPVCTDKPTHEKTTKIAC
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AKVACKSSQPDLDKNPASSKRRLKTSLGKVGVKEELLAVGKLTQTSGETTHTHTEPTG
DGKSMKAFMESPKQILDSAASLTGSKRQLRTPKGKSEVPEDLAGFIELFQTPSHTKES
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PKPAVGEEKDINTFLGTPVQKLDQPGNLPGSNRRLQTRKEKAGALEELTGFRELFQTP
CTDNPTADEKTTKKILCKSPQSDPADTPTNTKQRPKRSLKKADVEEEFLAFRKLTPSA
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ADGLQGETQLLVSRKSRPKSGGSGHAVAEPASPEQELDQNKGKGRDVESVQTPSKAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASFPLYEPAKMKTPVQYSQQONSPQKHKNKDLYTTGRRESVNLGKSEGFKAGDKTLTP
RKLSTRNRTPAKVEDAADSATKPENLSSKTRGSIPTDVEVLPTETEIHNEPFLTLMLT
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LQKRVSISRSQHDILQMICSKRRSGASEANLIVAKSWADVVKLGAKQTQTKVIKHGPQ
RSMNKRQRRPATPKKPVGEVHSQFSTGHANSPCTIIIGKAHTEKVHVPARPYRVLNNF
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LPTSESFGGNVFFSAQNAAKQPSDKCSASPPLRRQCIRENGNVAKTPRNTYKMTSLET
KTSDTETEPSKTVSTVNRSGRSTEFRNIQKLPVESKSEETNTEIVECILKRGQKATLL
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TELMKDTARGONLLQTQDHAKAPKSEKGKITKMPCQSLQPEPINTPTHTKQQLKASLG
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TSTKQRPKRSIRKADVEGELLACRNLMPSAGKAMHTPKPSVGEEKDIIIFVGTPVQKL
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DLAGFKELFQTPDHTEESTTDDKTTKIACKSPPPESMDTPTSTRRRPKTPLGKRDIVE
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H.sapiens gene for antigen of the monoclonal antibody K1-67.
X74107
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            Submitted (08-JAN-1996) J. Gerdes, Molecular Immunology,
Forschungszentrum Borstel, Parkallee 22, D- 23845, Borstel, FRG
2 (bases 1 to 14041)
                                                                          Sequence of the human Ki-67 protein gene 5' and promoter region Unpublished
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Duchrow,M., Schluter,C., Wohlenberg,C., Flad,H.D. and Gerdes,J.
Molecular characterization of the gene locus of the human cell proliferation-associated nuclear protein defined by monoclonal
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Matches 23; Conservative
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Direct Submission
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SOURCE
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TITLE
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Lierct Submission

AL Cambridgeshire, CBIO 18A, UK. E-mail enquiries.

Cambridgeshire, CBIO 18A, UK. E-mail enquiries.

Cambridgeshire, CBIO 18A, UK. E-mail enquiries.

I wing sequence assembly data is compared from overlapping clones.

Nov 16, 2001 this sequence version replaced gi:16151408.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL: Sw: SMISSPROT: Tr., TREMBL: WORMPEP: Information on the WORMPEP there is the content of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL355529 140466 bp DNA linear PRI 15-NOV-2001
Human DNA sequence from clone RPI1-85C15 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human corromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-85C15 is from the library RPCI-11.1 constructed by the group http://www.chori.org/bacpac/home.htm
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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28345. 28350
29576. 29581
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                                                                                                                                      14226. .14344
/product="antigen of the monoclonal antibody Ki-67"
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/product="antigen of the monoclonal antibody Ki-67"
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15738. .15893
/product="antigen of the monoclonal antibody Ki·67"
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17429. .1794
17795. .18794
17795. .18159
18160. .18586
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18587. .18889
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19253. .19618
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14345. .14454
/number=10
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25014. .27009
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27010. .29601
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14627. .15737
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15894. .16847
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21071. 21433
// Note="K1-67 no 11"
21800. 22165
// Note="K1-67 no 12"
// Note="K1-67 no 13"
22586. 22585
// Note="K1-67 no 14"
22586. 22882
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22883. 23339
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20718. 21070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus clone CH230-382H23, *** SEQUENCING IN PROGRESS
***, 67 unordered pieces.
A0125512
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                                                                                                                                                                                                                                                                                            /note="Tandem repeat. Forced join. Gap size estimated to be approximately 300bp by restriction digest" 30925 c 31089 g 41626 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                 /clone="RPI1-85C15"
//clone_lib="RPC1-11.1"
33521...33577
//note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                           /chromosome="10"
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doss/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                               Submitted (06-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 151959)
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 89991 bases at least Q40 Consensus quality: 97816 bases at least Q20 Consensus quality: 101398 bases at least Q20
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gap of unknown length
contig of 1681 bp in length
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contig of 1048 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Tracey, A.

Direct Submission

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Direct Submission

Direct Submission

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jan 24, 2002 this sequence version replaced gi:15020956.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >-

10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following, abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, NORMPEP; Information on the WORMPEP

Here of the overlap of the overlapping clone are databased can be found at the feature assembly was confirmed by the following the feature table with their source databases: Em:, EMBL; Wp:, NORMPEP; Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA sequence from clone RP11-140A10 on chromosome 10, complete sequence.
AL512622 AC024653
AL512622.9 GI:18369618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-140A10 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-140A10 is at 145630 in this sequence. The true right end of clone RP11-46A10 is at 2000 in this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl0 RPI1-140A10 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,

Brodanin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,

Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,

Haphjghi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,

Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, O.L., Maduro, V.B.,

Margulise, B.H., Masiello, C., Maskeri, B., Maskriian, S.D.,

McCloskey, J.C., McDowell, J., Paquirigan, C., Pearson, R.,

Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,

Wethertby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

In Unpublished
                                                                                                                                                                                                                                                          Despectation repeats from the approximated by a percentification digest data... 4711. 47315

Anote—'Sequence from overlapping clone RP13-449N13
(AL451056). Assembly confirmed by restriction digest... 47417. 47788

Anote—'Sequence from overlapping clone RP13-449N13
(AL451056). Assembly confirmed by restriction digest... 47761

Anote—'Weak data"

A7752. 47761

A77530. 48402

Anote—'Sequence from overlapping clone RP13-449N13
(AL451056). Assembly confirmed by restriction digest... 47810. 48402

Anote—'Sequence from overlapping clone RP13-449N13
(AL451056). Assembly confirmed by restriction digest... 60214

Anote—'Single clone region. Sequence from reads from a short insert library derived from a single puc clone. Restriction digest data confirm the assembly."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                      16591. 36708
note="Single clone region. Sequence from reads from a
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Submitted (24-MAY-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 135851)
                                                                                       short insert library derived from a single puc clone. Restriction digest data confirm the assembly." 36670. 36676 Anote-"Sequence from uni-directional dGTP big dye
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Papio cynocephalus anubis clone RP41-93A16, complete sequence.
ACO91714
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Pred. No. 2e+02;
); Mismatches 3; Indels 0;
                                                                                                                                                                                                                                           /note="Tandem repeat. Forced join.
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                    /clone_lib="RPCI-11.1"
36591. .36708
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Matches 20; Conservative
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Rattus norvegicus clone CH230-253F12, *** SEQUENCING IN PROGRESS A**, 62 unordered pieces.
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19284. .>135851

/note="this sequence is not the entire insert of clone RP41-93A16, clone overlaps with GenBank Accession Number AC091714 (nucleotides 1-63437) clone RP41-93A16 (center project name ccg); this annotated segment represents overlap with nucleotides 1-16583 of AC091714"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alstrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chowdhry, I., Christopoulos, C.,
Green, E.D.
Direct Submission
Submitted (20-AUG-2002) NIH Intramural Sequencing Center, 8717
Submitted (20-AUG-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Aug 20, 2002 this sequence version replaced gi:18464062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double-stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 135851;
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/sub_species="anubis"
/db_xref="taxon:9555"
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90.5%; Pred. No. 3.2e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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Center clone name: 093A16
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1. .135851
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NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Hu,P., Emanuel,B. and Roe,B.A.

Hu,P., Emanuel,B. and Roe,B.A.

Hu,P., Emanuel,B. and Roe,B.A.

Submitted (27-MAY-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

2 (bases 1 to 168239)

Hu,P., Emanuel,B. and Roe,B.A.

Direct Submission

Submitsion

Submitted (25-NOV-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens Chromosome 22q11 BAC Clone b444p24 In The BCRL2-GGT
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Homo sapiens chromosome 22q11 clone b444p24, complete sequence.
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AC006549 174840 bp DNA linear PRI 31-MAY-2000
Homo sapiens chromosome 22q11 clone p215k21, complete sequence.
AC006549
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2 (bases 1. C. 174840)
Hu, P., Chen, F., Dumanski, J. and Roe, B.A.
Direct Submission
Direct Submission
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                  OK 73019, USA.
(OK 73019, USA.
(Dases 1 to 168239)

Hu, P., Emanuel, B. and Roe, B.A.
Direct Submission
Submitted (09-MAR-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 (bases 1 to 168239)
Hu.P., Emanuel, B. and Roe, B.A.
Direct Submission
Submitted (Jal-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                            Submitted (26-NOV-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                   6 (bases 1 to 168239)
Hu,P., Emanuel,B. and Roe,B.A.
Direct Submission
Submitted (19-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 19, 2000 this sequence version replaced gi:7212014.

Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

ACOUG647(pi58119) 114717 179269 (0) overlaps ACOUG6316444p24) 1 64569 (103670) ACOUG097(p201m18) 102493 162269 (0) overlap ACOUG6316444p24) 1 6456 (0) overlap ACOUG6316444p24) 1 143072 (25167) ACOUG6316444p24) 1 164871 168239 (0) overlaps ACOL44p24) 1 143072 (25167) ACOUG63(b444p24) Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hu,P., Chen,F., Dumanski,J. and Roe,B.A.
Homo sapiens Chromosome 22q11 PAC Clone p215k21 Distal To DGCR
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/db_xref="taxon:9606"
Hu, P., Emanuel, B. and Roe, B.A. Direct Submission
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50533 c 49818
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Direct Submission

Submitted (04-NUG-1994) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other current sequence finishing criteria for the C. elegans genome sequence finishing criteria for the C. elegans genome sequence finishing criteria for the C. elegans genome sequence and open strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone T04A8. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The true left end of clone T04A8 is at 1 in this sequence. The true right end of clone T04A8 is at 4879 in sequence 235719.

The true right end of clone T23F11 is at 5962 in this sequence. The start of this sequence (1. .96) overlaps with the end of sequence
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   Direct Submission
Submitted (04-AUG-2000) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Aug 4, 2000 this sequence version replaced gi:9665183.
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HTG; 1,4-Alpha-glucan branching enzyme; 50S ribosomal protein L16; Andophosphoribosyltransferase; C-type lectin; calpain thiol protease; DNAJ; emb-5 gene; glucose-6-phosphate 1-dehydrogenase; Glutamine phosphoribosylpyrophosphate amidotransferase; elutamine triplet M protein; Non-histone chromosomal protein
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Caenorhabditis elegans cosmid T04A8, complete sequence.
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90.5%; Pred. No. 3.2e+02;
Live 0; Mismatches 2;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22q11"
/clone="b518b9"
a 55467 c 37478 g 37455
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Matches 19; Conservative
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (1-MAY-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
ON Mar 9, 2000 this sequence version replaced gi:6468071.
Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below. ACO06547(pi5819) 81952 179269 (0) overlapping regions below. ACO06549(p215k21) 1 97222 (77618) ACO00097(p201m18) 69724 162569 (0) overlaps ACO06549(p215k21) 32674 174840 (0) overlaps ACO0766319444224) 1 143072 (25167).
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                                                                                    Submitted (25-NOV-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-MAR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                            Submitted (26-NOV-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Homo sapiens chromosome 22q11 clone b518b9, complete sequence.
ACO58790
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90.5%; Pred. No. 3.2e+02;
iive 0; Mismatches 2; Indels
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Hu,P., Wu,H., Yang,L., Morrow,B.E. and Roe,B.A.
Direct Submission
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Hu,P., Wu,H., Yang,L., Morrow,B.E. and Roe,B.A.
3 (bases 1 to 174840)
Hu,P., Chen,F., Dumanski,J. and Roe,B.A.
Direct Submission
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Hu,P., Chen,F., Dumanski,J. and Roe,B.A.
Direct Submission
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Hu,P., Chen,F., Dumanski,J. and Roe,B.A.
Direct Submission
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Hu,P., Chen,F., Dumanski,J. and Roe,B.A.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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BASE COUNT

ORIGIN

FEATURES

Matches

ò

AC058790/c

Locus

ORGANISM

AUTHORS TITLE

JOURNAL AUTHORS

REFERENCE

REFERENCE

TITLE JOURNAL

AUTHORS

REFERENCE

```
join(11864...11952,12576. .12981,13028. .13288,13524. .13833,
13882. .13997,14293. .14457,14502. .14597)
/gene="T04A8.5"
                                                                                                                                                                                                                                                                                                                                             .13288,13524. .13833,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:022134"
/translation="MCGIFGIVAAGNYEHLNVLAANGLAALQHRGTESTGLVGSDGIT
RDHVEIIKGHGLVRDVITEDNISRANGQSIIIGHNRYSTAGKKKSGINCVQPFVVYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGTVAIAHNGELVDAKOKRKEVLHEGVGLSTDTDSELIAQMIAKAIALNVKCKYGQEM
GDITRELAVTWASALNMSYSLLVMTFDRLAIIRDFGRRELVGVGTVYSKROPEAFIAS
SEGGAFPANAKLDFPRYRGET VELSTGGIKSVWQMKDNTPLAMCIFEVVYFARNDSEI
EGQOVQTVREECGKTMALEDDLEADIVGNVPDSSLSAAIGYASOSGITYEPVLHNSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:022144"
/translation="MSDSDDNAYSDYLGNRRAALQKKRQPVRVCESDDSDDDFDTSGP
SPMRKKTRETQLFPDDSDDDECVEVEKETYSQKVRHEIDDVEEAYRRSIYKRETVIHA
                                                                                                                                                                      RPPPGSKTEARGIKAGVHVCREILFLCETIDSNADGEEPHKYVKFGKLFNIYSFYSDK
LVGMLIRARKYGLVHFEGEMLYQRQDDEKIITMLMSLQEIRESLTASGDPANCIQIRR
NSEPVAFVPPVSKEAPRPRPIRSDSVTSSKAKFEAPPPPNTDSLPVQGRPKKPWTPKD
                                                                                                                                                                                                                                                                             TSKAPIHLIRRMRLKIFMGLCLLCYTNAQVDRDWSFQQMCEFWGGEQTYRARNGYKVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGRGFIEPNDEMRONAIKMKFGVLKKKIHGORIVLVDDSIVRGNTMRTLVKMLRDAGA
KEVHLRIASPPVKFPCFMGINIPTTKELIAAEKTIPEICQFVGADSVRYLSVDGLVSS
VQKGIERAANFSPGHCTACLTGKYPVAIDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKELLGYFRQFGNVLRIRVARNRTGNHKGWAYVGFDNKAVAETAAESMNGYLMFEQR
LGCTVWKPELIPKAMRHGPLLVWRPSYLGIAKKDTIARNNTTGKNDVINAKKRVQNLN
                                                                                                                                          /translation="MPIGSASDTIRKFNAVAQANEEVLKKNPYSDTYKIQAFDTKNYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="wVAQNPTSISSGGRKQPQKQDKVQKKQLKKIYVVKIKRIPFGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTLKKLQNMGINYDFSVSGTPRTPLKKVIDNEYQFISDVTPKSTTPKIVKAATPRAAT
PKAVTPKQATPRVSTPVTKKVVIKTPKTEKPEPKQFTPRTRAGKKAAAAATPQAKSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(14747. .14836,14881. .15396,15445. .15558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(14747. .14836,14881. .15396,15445. .15558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains similarity to Pfam domain: PF00076 (RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Amidophosphoribosyltransferase (glutamine phosphoribosylpyrophosphate amidotransferase), contain spinaliarity to Pfam domain: PF00156 (Phosphoribosyl transferase domain), Score=15.0, E-value=0.0005, N=1; PF00310 (Glutamine amidotransferases class-III), Score=13.9, E-value=7.1e-46, N=1, /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recognition motif. (a.k.a. RRM, RBD, or RNP domain)), Score=57.0, E-value=1.3e-13, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(16523. .16784,16831. .17000,17047. .17601)
/gene="T04A8.8"
join(16523. .16784,16831. .17000,17047. .17601)
/gene="T04A8.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="cDNA EST yk339d3.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                         join(11864. .11952,12576. .12981,13028. .1
13882. .13997,14293. .14457,14502. .14597)
/gene="f04A8.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA EST yk222all.3 comes from this gene CDNA EST yk222all.5 comes from this gene CDNA EST yk432fl0.3 comes from this gene CDNA EST yk432fl0.5 comes from this gene CDNA EST yk497a8.3 comes from this gene CDNA EST yk497a8.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA EST yk339d3.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNTILKSVAASARPAAVEKKTLRSRGKKKSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:Q22135"
                                                                                                      /db_xref="SPTREMBL:Q22133"
                                   /protein_id="CAA84722.1"
/db_xref="GI:3879337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA84723.1"
/db_xref="G1:3879338"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA84724.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA84734.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:3879349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:3879339"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15604. .15807))
/gene="T04A8.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15604. .15807))
/gene="T04A8.6"
                                                                                                                                                                                                                                                                                                             IYDLSTDIMDLFN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                         join(285. .515,1092. .1310,1365. .1508,1567. .1749,1985. .2182)
/gene="T04A8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1749,1985. .2182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEVIPPESIDNNLISENTATION TRANSCRIPTION TRANSCRIPTION OF SVIFYTLYNUNDRICHTIAL STATES SVIFYTLYNULPRESIDNNLISENTATION SVIFYTLYNULPRESIDNNLISENTATION SVIFYTLYNULPRESIDNS TRANSCRIPTION COMPLEMENT (join (5293. . 5696, 5899. . 6660, 6234. . 6659, 67019. . 7072, 7227. . 7300))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLSSTCEDNVPYHINNAEASEVKTTCEAEATLICKSGWVQMFGRCYKITKTMMTRDKA
EEHCKNQQDHTSTIAFMHREALPFRWNDYFTRVSRIWMDASKVITNDLIYDVEGGNVL
                                                                                                                            the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FFVATILGLTMLKQRIKSAERSLTIVTMIMAVQTVTFASIQIYFVFFAAYTPKIRSVL
LQIVSFVFDSLYVFSPIALIVMSRQLRKDIFNLKDKETQISMYPNSEL"
joln(2532....2658, 2878...3338, 3506...3697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains similarity to Pfam domain: PF00059 (Lectin C-type domain), Score=9.2, E-value=0.0011, N=1" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALDGYKYNLPNVAIARVPKDETAMVLCEYTPPKTKSESNYLLRRYGEIYYPPLVTSE
SVYMRTTSSRIRNAEDPLADHNYCTELMKPVFRGGEAQSALPTQEFVKKLTGTNGFRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKRVKTGQLWCHKYVHDMSMNNDDAEKKCNDMGAHLSSFTTYEELKLLDEMILEVYPN
DNNIAVWLGAKRREECGDLSKNFTGGYSKDIHDPCARSRVFEWQNGVAQNPPIFVGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNSSRVVFPANFSYEDPLPFECNEDPNVVLSLAMYGMQSSYLIV
GAVLNVMIVYTVFHGNSYRDNSFYMLYCADAIVGIXINTAEVIFGRIFIYITPLCPIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPYFFTPSILTKMYYAALHYSLGFKTFSQIFMSFNRMTCVIFLMKHLKLWKQILKPVL
ITFILPLGVIWKILLSRVYINPNGAGFSVNYKDYFPWANISILHLFHFTLCFVLVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNILLLYTILFKNSEIYASSSFFLIYSTDCFVSFSMIFLDIIGRTLVYFTPLCPIIAP
MFYEPLIGFKIMMIVLHHSRACKSLIQILLVVNRMSCVIYPIRYGKMMMRPLKYLIIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFIDVTIVRTMLESHDIFKMRRNSTRWKVTNARSSFLRHRTMRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDYWAEKYEPNHSTDSERCLVQMSGSMSVWYGDNKPRNMQINDIYCNYEFKFLCGKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="See T23F11.5, contains similarity to Pfam domain: PF02118 (C.elegans Srg family integral membrane protein), Score=325.5, E-value=2e-94, N=1" /codon_start=1
For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                   This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(7871. .8071,8723. .8819,8916. .9181,
9228. .9359,9489. .9585,9638. .9714))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(5293. .5696,5899. .6060,6234. .6659,
6706. .6965,7019. .7072,7227. .7300))
/gene="T04A8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8819,8916. .9181,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains similarity to Pfam domain: PF02118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (C.elegans Srg family integral membrane protein),
Score=589.9, E-value=5.1e-174, N=1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(285. :515,1092. :1310,1365. :1508,1567.
/gene="T04A8:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Join(2532. .2658,2878. .3338,3506. .3697)
/gene="T04A8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(7871. .8071,8723. .88.
9228. .9359,9489. .9585,9638. .9714))
/gene="T04A8.4"
                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA84725.1"
/db_xref="GI:3879340"
/db_xref="SWISS-PROT:P46568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:022136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA84726.1"
/db_xref="GI:3879341"
                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                     /chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="T04A8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTFAVKKNL
                                                                   name=T04A8
IMPORTANT:
                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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AC127160
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 19;
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DEFINITION
                                                                                                                                                                                                                                     SASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 17
AC127160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                          ORIGIN
                                    ESHGNDMKSRHDIFLESTFSEIRRIYÄTKWGCPVSCVVFSHNGKTIDTYTTPOSLGWR
PWILDHPLIEASKEAGEPABYFTIENSPDSTTIKVLLASRRKPVQVBAAKDTTIQEIL
GKVIDAFVEDKEENIPSIESMKVYFDNERIKDVNITCEQLDLEDDDCIEVYF"
join (17889. . 18141, 18272. . 18953, 19001. . 19116, 19172. . 19654,
19718. . 20060, 20109. . 20277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usosophila melanogaster (subclones in sac irom Fi clone DS00b49)

(D167)) DNA.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Celniker, S. E., Aghavani, A., Arcaina, T. T., Baxter, E., Blazej, R.G., Chew, M., Doyle, C. M., Farfan, D. E., Flanagan, J., Houston, K.A.,

Hummasti, S. R., Karra, K., Kearney, L., Kim, S. H., Lee, B.,

Lomotan, M.A., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M.,

Nixon, K., Pacleb, J. M., Park, S., Pfeiffer, B., Punch, D., Snir, E.,

and Kimmel, B.

Sequencing of Drosophila chromosome 2R, region 53C1-53C2

London (1997)

Celniker, S. E., Aghavani, A., Arcaina, T. T., Baxter, E., Blazej, R.G.,

Chew, M., Doyle, C. M., Farfan, D. E., Flanagan, J., Houston, K.A.,

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Lomotan, M.A., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M.,

Nixon, K., Pacleb, J. M., Park, S., Pfeiffer, B., Punch, D., Snir, E.,

Twomey, B., Wan, K. H., Whitelaw, K. R., Yee, A., Zhang, R., Zieran, L.L.,

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Twomey, B., Wan, K. H., Whitelaw, K. R., Yee, R., Zheng, R., Zieran, L.L.,

Twomey, B., Wan, K. H., Whitelaw, K. R., Yee, R., Zieran, L.L.,

Twomey, B., Wan, K. H., Yee, R., Yee, R., Zieran, L.L.,
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This PI was assembled from the following subclones: 2_g6, 1_d5 (AC00319), 2_g7 (AC003132), 2_d1 (AC003132), 2_d2, 2_d3 (AC003132), 2_d2, 2_d3 (AC003132), 2_d2, 2_d3, 2_d3, 2_d3, 2_d3, 1_d11, 2_b8 (AC003321), 2_f5, 1_c3, 1_b9, 2_d9, 2_d1, 1_d12, 2_a7, 1_a9, 1_b12, 1_b12, 1_a1
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For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
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PVEKNNVISGLLKICEGWDEAAKSGAQPEVEDVKDDSDADESSIAAENFPVTVVILDC
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Submitted (28-FBB-1998) Berkeley Drosophila Genome Project, MS
Submitted (28-FBB-1998) Berkeley Drosophila Genome Project, MS
Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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86.4%; Pred. No. 6.2e+02;
.ive 0; Mismatches 3; Indels 0;
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RAISPROOKS, S. L., AMARATHURG, H. C., ARD-J. R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Shrever, C., Burrell, K. L., Byrd, N. C., Carron, T., Bowles, D., Barrell, K. L., Byrd, N. C., Coyle, M. Brown, B., Brown, M. C., Chen, G., Chen, G., Chen, G., Chen, R., Chen, G., Christopoulos, C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. L., David, R., Davila, M. L., David, R., J., Earnhart, C., Edgar, D., Erdwag, C.C., Elhj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhj, C., Escotto, M., Earnhart, C., Edgar, D., Flagg, N., Frort, J., Poster, P., Prants, P., Gorrell, J. H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harr, M., Halloway, C., Hollins, B., Hernandez, O., Hodgeson, M., Holloway, C., Howard, J., Ackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudh, S., Kovar, C., Li, J., Li, J., Li, Z., Lichearge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Marchine, M., Martin, R., Svatek, A., Tawor, R., Socott, G., Shoos, H., Sanch, H., Stanley, H., Stone, H., Sutcher, S., Soctt, G., Shoos, H., Sanch, R., San
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Pred. No. 6.3e+02;
0; Mismatches 3; Indels
/organism="Drosophila melanogaster"
                                                                                                    /map="53C1-53C2"
/clone="P1 DS00649 (D167)"
/note="Plate 6 and 7 - Stable 2"
22543 a 17463 c 17309 g 22345 t
                          /db_xref="taxon:7227"
/chromosome="2R"
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Direct Submission

TITLE

Location/Qualifiers 1. .79660

source

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HTG 20-JUN-2002
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/db_xref="taxon:10116"
/clone="CH230-460D14"
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NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                    Worley K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
               2. (bases 1 to 109185)
Worley-K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 109185)
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, Brown, A., Camarata, J., Campopiano, A., Changaro, E., Chararo, B., Choepel, Y., Candongelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Gardo-Plerre, N., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Ling, MacCean, C., Maratas, T., Levine, W., Illev, I., Johnson, R., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCarly, M., McEwan, P., McKernon, K., Marquis, N., Matthews, C., McCarly, M., Mihova, T., Mergan, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petter, R., Riebeck, M., Riley, R., Rise, C., Raymond, C., Retta, R., Riebeck, M., Riley, R., Schupback, R., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 127568)
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1 27057: contig of 27057 bp in length 27158 109603: contig of 82446 bp in length 109604 109703: gap of unknown length 109704 118983: contig of 9280 bp in length 118984 125506: contig of 6423 bp in length 119084 125506: contig of 6423 bp in length.
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/note="assembly_fragment
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    125506
    /organism="Felis catus"
/db_xref="taxon:9685"
    /clone="RP86-400G2"

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27158. .109603
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

I (bases 1 to 125506)

I (bases 1 to 125506)

Bachseley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Broks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., IdOl., J.R., Karlins, E., Laric, P., Lee-Lin, S.-O., Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pagulitigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Miggins, L., Young, A., Zhang, L.-H. and Green, E.D., M. M. Miggins, L., Young, A., Zhang, L.-H. and Green, E.D., M. M. M. Miggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contign has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                 Felis catus clone RP86-400G2, WORKING DRAFT SEQUENCE, 4 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Green, E.D. Direct Submission Direct Submission Submitted (21-JUL-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA (bases 1 to 125506)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-JUN-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 20, 2002 this sequence version replaced gi:14993724.
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* This sequence will be replaced
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Consensus quality: 124261 bases at least Q40
Consensus quality: 125088 bases at least Q20
Insert size: 110000; agarose-fp
Insert size: 125206; sum-of-contigs
Quality coverage: 9.88x in Q20 bases; sum-of-contigs
Quality coverage: 8.68x in Q20 bases; sum-of-contigs
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgrl.nlh.gov
Contact: project Information
Center project name: cfo
Center clone name: 400G02
                                                                                                           AC092732.2 GI:21490168
HTG; HTGS_PHASE2; HTGS_DRAFT.
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Length 125506;

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HTG 21-AUG-2002 *** SEQUENCING

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    Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Location/qualifiers
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49543 49642: gap of 100 bp
67855 67954: gap of 100 bp
67955 774191: contig of 6237 bp in length
67955 774191: contig of 6237 bp in length
74292 127568: contig of 53277 bp in length.
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/db_xref="taxon:9606"
/chromosome="17"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 154076) Sudbrak, R. Borzym, K., Kosiura, A., Rak, K., Omran, H., Lehrach, H. and Reinhardt, R.
                                                                                                                                                                                    AC017124 143450 bp DNA linear HTG 09-DEC-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
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Homo sapiens chromosome 3 clone BAC RPCI-11 1164K7 map 3q21, ***
SEQUENCING IN PROGRESS ***, 2 ordered pieces.
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Clone received from Resource Centre of the Human Genome Project at the Max-Planck-Institut for Molecular Genetics.

* NOTE: This is a "working draft" sequence. It currently

* consists of 2 contigs. Gaps between the contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville, MD, USA
This sequence was identified as CDM:10209560 by the submitter.
This sequence was identified as CDM:10209560 by the submitter.
* NOTE: Information on this record e-mail to fly@celera.com.
* This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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Adams, M. and Venter, J.C.
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2 (bases 1 to 154076)
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/organism="Homo sapiens"
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1. (bases 1 to 15436)

2. I (bases 1 to 15436)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks;S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Banks,T., Burch,J., Burch,P., Burkett,C., Burchly K., Bonnin,D., Buhay,C., Burch,P., Burkett,C., Burchly K., Bonnin,D., Buhay,C., Burch,P., Burkett,C., Burchly K., Chacko,J., Chavez,D., Chen,G., Chen,R., Chacko,J., Chavez,D., Chen,G., Coo,C., Coyle,M.D., Dathorne,S.R., David,R., C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gall,R., Gorcell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Jackson,L.B., Jacobson,B., Jackson,A., Hogues,M., Holloway,C., Jackson,L.B., Jacobson,B., Jackson,A., Hogues,M., Holloway,C., Lawis,L., Li,J., Li,Z., Licherige,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lietar,A., Lucier,R., Martindale,A., Matchell,T., Mohabbat,K., Matchell,T., Mohabbat,K., Mores,E., Mawkiney,E., Matchell,T., Mohabbat,K., Mores,S., Morgan,M., Moore,S., Moyer,N., Nguyen,N., Nguyen,P., Nguyen,P., Nguyen,P., Nguyen,P., Nguyen,P., Nguyen,P., Nguyen,P., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 149871: contig of 149871 bp in length 149972 154076: contig of 4105 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="3q21"
/clone="BAC RPCI-11 1164K7"
/clone_lib="RPCI-11 Human BAC library, originating
insitute: Roswell Park Cancer Institute"
/note="region between markers D3S3607-D3S1290"
a 29448 c 30349 g 48005 t 100 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 154076;
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are represented as runs of N. The order of the pieces
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86.4%; Pred. No. 6.4e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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Best Local
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AC117409
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KEYWORDS

VERSION

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standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STSs are identified using ePCR (Genome Res. 7:541-550) searches STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rives, M., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Suton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Vera, V., Villalon, D., Vinson, R., Wang, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, G., Ward-Moore, S., Walliamson, A., Washington, C., Watlington, S., Williams, G., Wu, C., Wu, Y., Williamson, A., Walsk, Wooden, S., Worley, K., Wu, C., Wu, Y., Wulliamson, A., Walsk, W., Wooden, S., Weinstock, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submitssion
Submitted (14-Aug-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 14, 2002 this sequence version replaced gi:21314809.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 154336)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANNOTATION OF FEATURES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1 to 154336)
Worley, K.C.
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/db_xref="taxon:9606"

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.397. .4400
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complement(17502. 17702)
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complement(1220...1635)
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complement(2056...2447)
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                                                                                                                                rpt_family-"L1ME"
695. 3071
                                                                                                                                                                                                                                                                                                                                                                                  note="UNSURE BASE C/CC
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                                                                                                                                                                                                             rpt_family="GA-rich"
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Homo sapiens 3q25-26 BAC CITB-243A6 (California Institute of Technology BAC Library) complete sequence.
AC008151 AC008171 G1:5629925
ATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 178242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Apylor Plaza, Houston, TX 77030, USA 4 (bases I to 178242) Worley, K.C.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                       Length 154336;
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                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                    Score 17.2; DB 9;
Pred. No. 6.4e+02;
0; Mismatches 3;
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                                                                                                                                      /rpt_family="MIR"
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complement(21627. .
                                                                                                                                                                                                                                                                     Db 41502 CCAAGCGTCTCATGAGCCACAT 41523
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.19530
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86.4%;
                                                                                                                                                                                                                               Conservative
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Direct Submission
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19510.
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                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
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JOURNAL
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                      RESULT 23
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                                                                                                                                                                                                                                                                                                                                 AC008151
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AUTHORS

(bases 1 to 178242)

Worley, K.C

REFERENCE AUTHORS

JOURNAL

TITLE

TITLE JOURNAL

Worley, K.C.

AUTHORS TITLE

REFERENCE

JOURNAL

Direct Submission

Worley, K.C.

AUTHORS

JOURNAL

COMMENT

REFERENCE

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cctggccaac(a)aggtgaaacc
ctggccaaca(a)ggtgaaaccc
ttagcccggg(c)gtggtggctaat
agcccgggcg(t)ggtgggccaat
attatatagg(t)gggaaccaat
gagctatgg(g)aaaagacagt
cagtaggg(g)aaaagacagt
                                                ttgccctcgg(c)ccccggcggccaggctgaa
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                        Edited+Context
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Consensus changing edits
                                                                                                                                                                            agcccgggng(n)ggtggctaat
attatatagg(n)gggacccatg
gagctatggg(n)aaaagacagt
cagtagcgcc(t)aaaactcctg
                                                   ttgccctcgg(n)ccccggcggccagccggcggccagcctggcc(n)actnggtgaa
                                                                                                                           ctggccnact(n)ggtgaaacccttagcccggg(n)gnggtggcta
                                                                                                                                                                                                                                                                                       tttttttt(n)gatacagggt
                                                                                                      cctggccnac(t)nggtgaaacc
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3q55-26"
/clone="CITB-243A6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family~"MLT1C"
577. .271.
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176, .7400
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/rpt_family="MLT1C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6261)
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/rpt_famlly="MER5B"
complement(378..413)
/rpt_famlly="MER102"
complement(455..765)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="MER45B"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(TG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MLT1F"
complement(6301..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family-"MLT1D"
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1531. .1722
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/rpt_family="MIR"
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7486. .7735
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/rpt_family="L2"
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3768. .3916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Feptrs of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on or before Jun 13, 2000 this sequence version replaced g1:5668751, g1:5668753.

INFORMATION: http://www.hgsc.bcm.tmc.edu/or email gc-help@bcm.tmc.edu
                  Submitted (22-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 178242)
                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (13-JUN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 178242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                      Department
                                                                                                                                                      Direct Submission
Submitted (09-00T-1999) Human Genome Sequencing Center, Departmer
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus:
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S (bases 1 to 185425)

S (cliker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A. Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, J.W., Firse, E. Galle, R.F., Gargy, N.S., George, R.A.,
Ferriera, S., Frise, E. Galle, R.F., Gargy, N.S., George, R.A.,
Ibeyam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, C., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveři, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC099027 185425 bp DNA linear INV 08-NOV-2001 Drosophila melanogaster, chromosome 2R, region 53C-53D, BAC clone BACR06115, complete sequence.
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                      join(8735. .8895,20435. .21674)
/gene="Homo sapiens caveolin-3 (CAV3) mRNA, complete cds, AF043101 and AF036365"
join(8741. .8895,52375. .52434,116209. .116631)
/gene="Unigene cluster containing AA448334 and AA452471"
/rpt_family="AluJb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and relationship to other sequences, please visit our sequence
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                                                                                                                                                                                                                                                                                                                      Score 17.2; DB 9; Length 178242;
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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Drosophila melanogaster
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AC099027.1 GI:16798959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
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AC122284 194991 bp DNA linear HTG 23-MAY-2002 Mus musculus chromosome UNK clone RP23-246A5, WORKING DRAFT SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                /clone="BACR06115 (D1338)"
/clone_lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 185425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-primer ET; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 190912 bases at least Q40 Consensus quality: 192510 bases at least Q30 Consensus quality: 19357 bases at least Q30 Insert size: 204000; agarose-fp Insert size: 19594; sum-of-contigs Quality coverage: 11.70 in Q20 bases; agarose-fp Quality coverage: 6.63 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web Site.http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 0% Sequencing vector: plasmid; 100%
                                                                                               /organism="Drosophila melanogaster"
/strain="y, cn bw sp"
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/chromosome="28"
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Pred. No. 6.4e+02;
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McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
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McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: M_BA0246A05
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86.4%;
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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5100. .6465
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9642. .13055
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clone_end:SP6
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42930 c 41683 g 53332 t
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'note="assembly_name:Contig47"
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Corganism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-246A5"
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1273: gap of u
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3693: gap of u
4999: contig o
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ORIGIN
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74.8%; Score 17.2; DB 2; Length 194991;

Query Match

Search completed: December 2, 2002, 22:01:00 Job time: 3434 secs

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Human bone marrow Probe #8570 for ge Probe #1245 used Human genome-deriv Human secreted pro Drosophila melanog

genome-deriv foetal liver #9296 for ge brain expres

Probe Human

#25308 used

Human secreted pro Human secreted pro Primer specific fo Borna disease viru Human cDNA encodin Human polynucleoti

Human signal pepti DNA encoding a CD4 Human PRO263 homol

Protein PRO263 cDN Human PRO263 cDNA. Human PRO263 cDNA. Human angiogenesis Mouse truncated be

Human PRÖ263

Human polynucleoti

Human reproductive Human secreted exp Human secreted pro

Drosophila melanog Bacillus lichenifo Human DNase I gene

Human reproductive

pro

Human secreted

Title: Perfect score:

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Sequence:

OM nucleic

Run on:

Scoring table:

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Minimum DB Maximum DB

Database

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Melanoma; thyroid tumour; MEL3; MEL7; Thy5; Thy11; Thy14; Thy15; rectal cancer; lung cancer; breast cancer; colon cancer; antibody Ki-67; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequence encoding the antigen of monoclonal antibody Ki-67
                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                            AAX41003
AAX51631
AAC16890
AAX41156
AAF94017
                                                                                                                                                                                                                              AAF61225
AAF93818
AAK51821
AAZ98172
AAV22687
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ABL88087
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RODNIN N.
FILONENKO V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATSUKA G.
SCANLAN M.
OLD L.
BILYNSKY B.
 WO200050595-A2.
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AAA64659;
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Probe #17588 for g
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2. \SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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                                                                                                                                                                                                          2059836
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     2185239 seqs, 1125999159 residues
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SCANLAN M.
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Matches 23; Conserv
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Bilynsky B;
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                                                                                                                                                   The specification describes polynucleotides which are associated with melanoma and thyroid tumors. Specifically, these are MELJ, MELJ, Thy5, Thy6, Thy11, Thy14, and Thy15. The polynucleotides are useful for diagnosing and treating a patient with melanoma, thyroid tumour, rectal cancer, lung cancer, breast cancer or colon cancer. The present sequence represents a polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell cycle protein; Ki-67; therapy; cell proliferation; allergy; tumor treatment; autoimmune disease; scar formation; inflammation; rheumatic disease; transplantation; ds.
                                                                         Novel isolated nucleic acid molecules for diagnosing and treating melanoma, thyroid tumors, rectal, lung, breast and colon cancers
 Old L;
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                                                                                                                                                                                                                                                                                          100.0%; Score 23; DB 21; Length 11435; 100.0%; Pred. No. 0.19; 1. Indels 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                               Sequence 11435 BP; 3802 A; 2828 C; 2684 G; 2121 T; 0 other;
 Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BORS-) FORSCHUNGSZENTRUM BORSTEL ZENT MEDIZIN.
 Matsuka G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 5-19; 36pp; German.
                                                                                                                      Claim 17; Page 81-85; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
197..9967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cell cycle protein Ki-67 DNA
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/product- "Ki-67"
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Rodnin N, Filonenko V,
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ID AA243872 standard; DNA; 12493
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Best Local Similarity 100.
Matches 23; Conservative
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                                              WPI; 2000-572092/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerdes J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY50976
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Gout I, Rod
Bilynsky B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ43872;
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treatment of tumors, autoimmune diseases, scar formation, inflammation, allergy, rheumatic diseases and defence against transplantation. This sequence encodes the human cell cycle protein K1-67 which is described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melanoma; thyroid tumour; MEL3; MEL7; Thy5; Thy11; Thy14; Thy15; rectal cancer; lung cancer; breast cancer; colon cancer; antibody Ki-67; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequence encoding the antigen of monoclonal antibody Ki-57.
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                                                                                                                                                                                                      100.0%; Score 23; DB 21; Length 12493; 100.0%; Pred. No. 0.19;
                                                                                                                                               Sequence 12493 BP; 4143 A; 3048 C; 2929 G; 2373 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecules for diagnosing and melanoma, thyroid tumors, rectal, lung, breast and colon
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                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodnin N, Filonenko V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA64658 standard; cDNA; 12515 BP
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                                                                                              the method of the invention.
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Best Local Similarity 100.0
Matches 23; Conservative
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in capression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70180), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the structure and/or cancer such as colon, breast, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell cancer infiltrating ductal cancer, and cancer and cancer
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                                                                                                                                                                                                         Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoma, papillary carcinoma and Wilm's tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 7459; 44pp; English
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2000US-0207456.
2000US-0608408.
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     Weaver Z;
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                                                                                                       WPI; 2002-188264/24.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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23;
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26-MAY-2000;
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Soppet DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
h; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
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219 ACCAGGCGTCTCGTGGCCACAT 197
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ID ABL69122 standard; DNA; 12515
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2000US-235863P.
2000US-236028P.
2000US-236032P.
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2000US-236109P.
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2000US-236891P.
2000US-237172P.
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2000US-237278P.
2000US-237294P.
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20-SEP-2000;
22-SEP-2000;
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18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
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27-SEP-2000;
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03-OCT-2000;
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Gaps

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Indels

Length 189;

DB 22; 'n.

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monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe SEQ ID NO: 24635.
                                                                                                                                  Sequence 189 BP; 52 A; 57 C; 40 G; 40 T; 0 other;
                                                                                                                                                                  Score 17.2; DE
Pred. No. 84;
0; Mismatches
                                                                                             at ftp.wipo.int/pub/published_pct_sequences
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-023659.
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86.4%;
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86.4%;
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                                                                                                                                                       Query Match
Best Local Similarity
.....hes 19; Conserva
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Best Local Similarity
Matches 19; Conserv
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                         The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
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   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                                                                                                                                                                                                                   Length 189;
                                                         Claim 4; SEQ ID NO 24271; 639pp + sequence listing; English.
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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86.4%;
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30-JUN-2000; 2000US-0608408.
03-MG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                     Query Match
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ABA40530
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                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                        Example 4; SEQ ID NO: 24635; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 189 BP; 52 A; 57 C; 40 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 84;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #25308 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
   Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                    analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 189 BP; 52 A; 57 C; 40 G; 40 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID No 17588; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                  Rank DR
                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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86.4%;
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                                                                                                                                                 30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 86.4 ses 19; Conservative
                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder;
                    cervical cancer;
                                                                                WO200157278-A2
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                   Homo sapiens
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                                                                                                                                                                                                                  30-JUN-2000;
                                                                                                                                                                                   04-FEB-2000;
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                                                                                                                09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #17588 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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Pred. No. 84;
0; Mismatches
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ACCAGGCGTCTCGTGGGCCACA 22
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0623366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.8%;
86.4%;
                  AAK50641 standard; DNA; 189
                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488900/53.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                              WO200157276-A2
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                              06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon probe ORF from lung SEQ ID No 24108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.2; DB 22; Length 189;
Pred. No. 84;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 189 BP; 52 A; 57 C; 40 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                             analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID No 25308; 654pp; English.
                                                                                                                                                                                                                  Rank DR;
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                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                  Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.8%;
                                                              03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                            2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
                                                                                                                                                                                                                                                          WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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03-AUG-2000;
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04-OCT-2000;
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                                                                                                                                                                                                                Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABS24117;
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ABS24117
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The higherland relates to a spatially-ductessable set on sample derived conclete acid probes having one cide from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of complements or the 1387 open reading frames derived from the 12614 onclete acid sequences mentioned in the specification, or their complements or the 1387 open reading frames derived from the 12614 or probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (b) contacting pecific hybridisting the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the atray; identifying exons in a eukaryotic genome, comprising (a) identifying exons from genomic sequences of the above mentioned microarray; assigning exons to a single exon probe; labeled nucleic acids from eukaryote lung mRNA, to a single exon probe; comprising (a) identifying exons from genomic sequence by the method in the above mentioned microarray; assigning exons to a single exon probe; comprising (a) identifying exons from genomic sequence by the method in the above mentioned microarray; assigning exons to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression analysis, and for identifying exons to a single exon or composition in the above mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, pulmonary high exons to a single exon in the problem reading frames (ORP). The
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                                                                                                                                                                                                                                                                                                              The invention relates to a spatially-addressable set of single exon
                                                                                                                             Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #11939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 189 BP; 52 A; 57 C; 40 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                         Claim 4; SEQ ID No 24108; 634pp; English.
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Rank DR;
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Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACCATGGGTCACGTGGGCCACA
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DK,
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Best Local Similarity
Matches 19; Conserv
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SG,
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Penn SG, Hanzel DK,
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                                                                                                WPI; 2001-488899/53
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        03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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03-AUG-2000;
21-SEP-2000;
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04-OCT-2000;
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AAK12157
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                                                                                                                                                                                                                                                                                           measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                  probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #9296 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.2; DB 22; Length 573; Pred. No. 90; 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 11939; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 573 BP; 147 A; 162 C; 116 G; 148 T; 0 other;
                                                                                                                                                                                         Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                         Hanzel DK, Chen W,
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Best Local Similarity 86.4%;
Matches 19; Conservative (
                                                                                    04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-ANG-2000; 2000US-023366.
21-SEP-2000; 2000US-0234687.
                                                                                                                                       27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                  30-JAN-2001; 2001WO-US00669
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2000US-0207456
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                           WO200157277-A2
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         Homo sapiens.
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26-MAY-2000;
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                                                09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID NO: 12148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 573 BP; 147 A; 162 C; 116 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 9296; 530pp; English
                                                                                                                                                                                                               Chen W, Rank DR;
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                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
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86.4%;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456
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Gaps

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Indels

Length 573;

DB 22; 3,

Score 17.2; DE Pred. No. 90; 0; Mismatches

74.8%; 86.4%;

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BP.

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Probe #8570 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; microarray; gene expression; cervical epithelial cell;
                                           Sequence 573 BP; 147 A; 162 C; 116 G; 148 T; 0 other;
                                                                                                                                                                                                 267 ACCATGGGTCACGTGGGCCACA 288
                                                                                                                                                                            1 ACCAGGCGTCTCGTGGGCCACA 22
the probes of the invention.
                                                                                                                                                                                                                                                                                                                                  AAI18637 standard; DNA; 573
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer; ss
                                                                                                          Local Similarity
nes 19; Conserv
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                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 12432; 658pp + Sequence Listing; English.
                                                                                                                                                        Example 4; SEQ ID NO: 12148; 650pp + Sequence Listing; English.
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Pred. No. 90;
0; Mismatches
    Rank DR
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
    Chen W,
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Best Local Similarity 86.4%;
Matches 19; Conservative
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    Hanzel DK,
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                                           WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                                       invention.
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    Penn SG,
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                                                                                                               brains
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 8570; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                Rank DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                           26-MAY-2000; 20000S-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632566.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                Chen W,
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30-JAN-2001; 2001WO-US00670
                                                      2000US-0180312
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Matches 19; Conservative
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                                                                                     Probe #12435 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
chronic Obstructive pulmonary disease; interstitial lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclenosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon probe from lung SEQ ID No 11863
                                                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 573 BP; 147 A; 162 C; 116 G; 148 T; 0 other;
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86.4%; Pred. No. 90;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID No 12435; 654pp; English.
                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 ACCATGGGTCACGTGGGCCACA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABS11872 standard; DNA; 573 BP.
                                AAI43749 standard; DNA; 573 BP
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2000US-0608408.
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                                                                    (first entry)
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les 19; Conserv
                                                                                                                                                   WO200157272-A2
                                                                                                                                  Homo sapiens.
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                                                                    17-0CT-2001
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                                                  AAI43749;
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               RESULT 17
                         AA143749
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a concleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with carray; identifying exons in a eukaryotic genome, comprising captithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably bound to each probe of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon from probe; in the above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single exon comprising one the exons should be assigned to a single gene, and cor all types using hybridisation to a single exon context the exons should be assigned to a single gene, approbes/open reading frames (ORF). The probes are used for gene corression analysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung diseases (CCOPP), interstitial lung disease (ILD), familial idiopathic pulmonary disease (CCOPP), interstitial lung disease (ILD), familial idiopathic pulmonary disease.
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Note: The sequence data for this patent did not form part for the present general directly from WIPO at the vibro-lint/pub/published_pct_sequences.
                                    pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
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Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measure gene expression in human lung samples
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21-SEP-2000; 2000US-234687P-
27-SEP-2000; 2000US-236359P-
04-OCT-2000; 2000GB-0024263.
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2000US-0608408.
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30-JUN-2000;
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us-09-700-906a-3.rng

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interactions
                                                                                                                                                     Local Similar
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                                                                                                                                                                                                                                                                                                                                   Drosophila;
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                                                                                                                                                   Query Match
                                                                                                                                                                     Matches
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                                                                                                                                                                                                         Human; secreted protein; cancer; tumour; developmental abnormality; foctal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alaheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atheroscierosis; diabeters; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AlDS; leukaemia; therapy; chromosome 10; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was found to be present on human chromosome 10. AAY76124 to AAY76223 represent the secreted proteins encoded by the 97 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptides they encode,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                          DB 24; Length 573;
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Wer LA, Soppet DR;
                                              Indels
        BP; 147 A; 162 C; 116 G; 148 T; 0 other;
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Wei F, Brewer LA,
                                             3;
                                             Mismatches
                          Score 17.2;
Pred. No. 90;
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                                                                          267 ACCATGGGTCACGTGGGCCACA 288
                                                                                                                                AAZ65257 standard; DNA; 1143 BP
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                                                                                                                                                                                         Human secreted protein gene 8.
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980S-0085920.
980S-0085921.
980S-0085923.
980S-0085923.
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98US-0085105.
98US-0085180.
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                           74.8%;
86.4%;
                                                                1 ACCAGGCGTCTCGTGGGCCACA
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                                              Conservative
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                                    Local Similarity
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        Sequence 573
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12-MAY-1998
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(ABB57737-ABB72072).

The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foctal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY76224 to AAY76424 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster expressed polynucleotide SEQ ID NO 17183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1143 BP; 242 A; 339 C; 351 G; 210 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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Pred. No. 94;
0; Mismatches
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ABL07567 standard; cDNA; 1851
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86.48;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABB63464
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 17180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                         ;
0
                                                      DB 23; Length 1851;
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86.4%; Pred. No. 1.1e+02;
tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 17180; 21pp + Sequence Listing; English.
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                                                                                                         Indels
Sequence 1851 BP; 479 A; 533 C; 478 G; 361 T; 0 other;
                                                                                                         3,
                                                Score 17.2; DI
Pred. No. 97;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     ABL07566 standard; cDNA; 7832 BP.
                                                                                                                                                                                           1361 CCGGACGTCTCGTTGGCCACAT 1340
                                                                                                         ;
                                                                                                                                                         2 CCAGGCGTCTCGTGGGCCACAT 23
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                                                   74.8%;
86.4%;
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11-JUL-2000; 2000US-0614150.
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                                                                          Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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P-PSDB; ABB63463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                           ABL07566;
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                                                      Query Match
                                                                                                                                                                                                                                                                                               RESULT 21
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colleted from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cells relative to expression of the same genes or one more second Bacillus cells. The method is useful for monitoring new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, cenvironmental stress or other physiological provocation. Extensive collow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
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Pred. No. 1.5e+02;
); Mismatches 2; Indels 0;
                                                                                                                                                                    Differential gene expression; genomic sequenced tag; GST; altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                 Bacillus licheniformis genomic sequence tag (GST) #249.
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90.0%;
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nes 18; Conserv
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Gaps

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RESULT 22

2 CCAGGCGTCTCGTGGGCCACAT 23

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Conservative

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Best Local Matches

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Homo sapiens.
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                                                                                               04-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                       genomic DNA library; another portion codon of the human Dwase I gene. It forms part of a DNA clone isolated from a human leukocyte genomic DNA library; another portion of the clone, comprising part of the 5' untranslated region and coding sequence of the TPO gene. Is given in AAT35523. Non-coding genomic sequences, e.g. exon 1, within and upstream of the transcribed regions of the Dwase I gene may be used as targeting sequences in DNA constructs useful for gene activation by homologous recombination. Novel genes are generated in which exogenous and endogenous sexons are operatively linked. Expression of Dwase I encoded by the endogenous gene can be activated in the trachea and lungs of a cystic fibrosis patient,
                                                                                                                                                                                                                                                                                                                                                                               genomic DNA fragment (AAT35522) corresponds to nucleotides -4512
                                                                                                                                                                                                                                                                                                                Altering expression of genes encoding thrombopoietin, DNase I or beta-interferon - using DNA constructs useful in gene therapy to treat, e.g. cystic fibrosis and multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%; Score 16.8; DB 17; Length 4042; 90.0%; Pred. No. 1.6e+02; 1.ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human reproductive system related antigen DNA SEQ ID NO: 9766.
                                                                                                        Gene targeting; gene activation; homologous recombination; DNase I; cystic fibrosis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4042 BP; 971 A; 1081 C; 1110 G; 878 T; 2 other;
                                                                                                                                                                                                                                                                      Selden RF, Treco DA;
                                                                                    Human DNase I gene 5' flanking sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thereby relieving respiratory distress.
                                                                                                                                                                                                                                                                                                                                                         Claim 27; Fig 10A-D; 115pp; English.
                                                                                                                                                                                                                                                  (TRAN-) TRANSKARYOTIC THERAPIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL07078 standard; DNA; 25701 BP
                     AAT35522 standard; DNA; 4042 BP.
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                                                                (first entry)
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                                                                                                                                                                                                                                                                       Hauge BM, Heartlein MW,
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Best Local Similarity
Matches 18; Conserval
                                                                                                                                                                                                                                                                                           WPI; 1996-443186/44.
                                                                                                                                                                                                                             17-MAR-1995;
                                                                                                                                                              WO9629411-A1
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                                                                                                                                          Homo sapiens
                                                              14-JAN-1997
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RESULT 23
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2000US-0189874
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WO200155320-A2
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Ruben SM;

Barash SC,

Rosen CA,

WPI; 2001-465570/50.

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2000US-0239937.
2000US-0240960.
2000US-0241231.
2000US-0241785.
2000US-0241786.
2000US-0241786.
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2000US-0251856.
2000US-0251868.
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                                                                                    2000US-0236370.
                                                                                                 2000US-0236802.
2000US-0237037.
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2000US-0237039
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2000US-0246523
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2000US-0254097.
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                        29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SE
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                73.0%; Score 16.8; DB 22; Length 25701; 90.0%; Pred. No. 1.8e+02; Live 0; Mismatches 2; Indels 0;
                                                                                                    Disclosure; SEQ ID NO 9766; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human reproductive system related antigen DNA SEQ ID NO: 9765
                                                                                                                                                                                                        Sequence 25701 BP; 6452 A; 7118 C; 6915 G; 5216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                            AAL07077 standard; DNA; 25758
                                                                                                                                                                                                                                                                                                 317 CAGGCGTGTCCTGGGCCACA 336
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2000US-019123
2000US-0209467
2000US-0214886
2000US-0215135
2000US-0216880
2000US-021680
                                                                                                                                                                                                                                                                                     3 CAGGCGTCTCGTGGGCCACA 22
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2000US-0186350.
2000US-0189874.
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2000US-0225266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0225267
2000US-0225268
                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-2001 (first entry)
                                                                                                                                                                                                                                             Local Similarity 90.0 nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04 - FEB - 2000;
24 - FEB - 2000;
16 - MAR - 2000;
17 - MAR - 2000;
18 - MAR - 2000;
19 - MAY - 2000;
20 - JUN - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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14-AUG-2000;
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Matches
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ID AAL
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PR 14-AUG-2000, 2000US-0255270.
PR 14-AUG-2000, 2000US-0225751.
PR 14-AUG-2000, 2000US-0225751.
PR 14-AUG-2000, 2000US-0225751.
PR 12-AUG-2000, 2000US-0225751.
PR 22-AUG-2000, 2000US-0226681.
PR 22-AUG-2000, 2000US-0226681.
PR 22-AUG-2000, 2000US-0226681.
PR 23-AUG-2000, 2000US-0227182.
PR 23-AUG-2000, 2000US-022831.
PR 12-EP-2000, 2000US-022931.
PR 01-SEP-2000, 2000US-023931.
PR 01-SEP-2000, 2000US-0233399.
PR 14-SEP-2000, 2000US-0233399.
PR 25-SEP-2000, 2000US-0233399.
PR 25-SEP-2000, 2000US-0233399.
PR 25-SEP-2000, 2000US-0233399.
PR 21-SEP-2000, 2000US-0233399.
PR 21-SEP-2
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 9765; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25758 BP; 6456 A; 7140 C; 6936 G; 5226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.0%; Score 16.8; DB 22; 90.0%; Pred. No. 1.8e+02; 1ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002, 21:02:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGCGTGTCCTGGGCCACA 336
         2000US-0246532
2000US-0246610
2000US-0246611
2000US-0249207
2000US-0249207
2000US-0249210
2000US-0249211
2000US-0249211
2000US-0249212
2000US-0249213
2000US-0249214
2000US-0249214
2000US-0249214
2000US-0249214
2000US-0249216
2000US-024926
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2000US-0254097.
2001US-0259678.
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Les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: December
Job time: 285 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465570/50
                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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Matches
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December 2, 2002, 20:56:18; Search time 50 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Run on:

(without alignments)
141.071 Million cell updates/sec

US-09-700-906A-3 23 1 accaggcgtctcgtgggccacat 23 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

441362 segs, 153338381 residues Searched:

Total number of hits satisfying chosen parameters:

239980

Minimum DB seq length: 66 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:* Issued_Patents_NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 64, Appl Sequence 13, Appl Sequence 146, Appl Sequence 1, Appli Sequence 1, Appli Sequence 567, Appl Sequence 567, Appl Sequence 569, Appl Sequence 180, Appl Sequence 180, Appl Sequence 38, Appl Sequence 2, Appli Sequence 38, Appl Sequence 1, Appli Sequence 1, Appli	Sequence 73, Appl
US-09-232-201-64 US-08-888-077A-33 US-08-484-9708-146 PCT-US92-01358-1 US-08-275-916-1 US-09-641-638-566 US-09-641-638-568 US-09-641-638-568 US-09-641-638-568 US-09-641-638-569 US-09-641-638-569 US-08-658-665-38 US-08-68-665-38 US-08-485-665-38 US-08-485-665-38 US-08-485-665-38 US-08-485-665-38 US-08-485-665-38 US-08-485-665-38 US-08-485-665-38 US-08-796-101-2 US-08-796-101-37	US-09-085-273-73
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0.02020202020204666 0.0202020202020202020	15.2
2000 2000	45
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Belden, Richard F
TITLE OF INVENTION: Protein Production and Delivery
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STAPE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,030A
FILING DATE: 17. MR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,188
FILING DATE: 05-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11704
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09627
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,391
FILING DATE: 13-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,586
FILING DATE: 03-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/911,533
FILING DATE: 10-7UL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,840
FILING DATE: 05-NOV-1991
                       ; Sequence 17, Application US/08406030A; Patent No. 6270989
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 17 CLASSIFICATION:
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US-08-406-030A-17
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US-08-369-822C-1/c
Sequence 1, Application US/08369822C
Patent No. 6015660
GENERAL INFORMATION:
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; Patent No. 6077510
                   160 ACCAGGAGCCTCGTGGTCCAGAT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCAGGCGTCTCGTGGGCCACAT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 865 South F
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017-2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Lipkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-582-776C-1/c
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CO44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: IIOO NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                               Query Match 73.0%; Score 16.8; EBest Local Similarity 90.0%; Pred. No. 29; Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.2%; Score 16.6; I 82.6%; Pred. No. 33; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,688
ER: 1488.0490001
               REFERENCE/DOCKET NUMBER: TKT95-01
TELECOMMUNICATION INPORMATION:
TELEPAX: (617) 861-640
TELEFAX: (617) 861-9540
INPORMATION FOR SEQ ID NO: 17:
SEGURNCE CHARACTERISTICS:
LENGTH: 4042 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-08-892-880-12/c
; Sequence 12, Application US/08892880
; Patent No. 5942417
                                                                                                                                                                                                                                                                                                                                                                   3550 CAGGCGTGTCCTGGGCCACA 3569
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                               3 CAGGCGTCTCGTGGGCCACA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                          single
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                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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US-08-892-880-12
                                                                                                                                                                                                                            US-08-406-030A-17
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1 ACCAGGCGTCTCGTGGGCCACAT 23

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APPLICANT: Lipkin, W. I.
APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Kliche, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneemann, Anette
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: Borna Diseases
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                     E: Fulbright & Jaworski, L.L.P.
865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,822C
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A. (Ph.D.)
REGISTRATION NUBER: 39,94
REFERENCE/DOCKET NUMBER: 1279-194XX
TELECOMMUNICATION INFORMATION:
TELEPHNE: 213/690-4518
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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82.6%; Pred. No. 34
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Briese, Thomas
Kliche, Stefanie
Schneider, Patrick A.
Stitz, Lothar
Schneemann, Anette
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 13, Application US/09232160

Patent No. 6368794
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Steve Daniel
APPLICANT: Steve Daniel
APPLICANT: Steve Daniel
APPLICANT: Laura Stuart
APP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCIT (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,831B
FILING DATE: 04-MAY-1995
CLASSIECATION 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.2%; Score 16.6; D
82.6%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.2%; Score 16.6; D
82.6%; Pred. No. 35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                              PULGASJELIZATION
PULGATION DATA:
PULGATION DATA:
APPLICATION NUMBER: US 08/369,822
FILING DATE: 06-74N-1995
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A. (Ph.D.)
REGIGTRATION NUMBER: 39,944
REPERENCE/DOCKET NUMBER: 1279-194C1
TELECOMMUNICATION INFORMATION:
TELEFONE 213/680-9200
TELEFONE 213/680-4518
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 1112 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 ACCAGGAGCCTCGTGGTCCAGAT 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 ACCAGGCGTCTCTTGGGTGGCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA to mRNA
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.2°
Best Local Similarity 82.6
Matches 19; Conservative
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US-09-232-160-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                90017-2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-232-160-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: -
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APPLICANT: Lipkin, W. I.
APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Riche, Stefanie
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
Borna Disease Viral Sequences,
Diagnostics and Therapeutics for Central Nervous
System Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                   ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: California
STATE: California
ZIP: 90017-2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IND PC COMPUTED:
COMPUTER: IND PC COMPUTED:
COMPUTER: IND PC COMPUTED:
COMPUTED: SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
PRICE APPLICATION NUMBER: US/08/582,776C
FILING DATE: 04-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/369,822
FILING DATE: 06-JAN-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/434,831
FILING DATE: 04-MAY-1995
ATTORNEY FAGENT INFORMATION:
NAME: CHURCHILL, MAIGATER
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 39,944
TELECOMMUNICATION INFORMATION:
TELECHONE: 213/892-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.6;
Pred. No. 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACCAGGGGTCTCGTGGGCCACAT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 ACCAGGCGTCTCTTGGGTGGCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.2%;
82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1112 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
            TITLE OF INVENTION: BOY TITLE OF INVENTION: DIA TITLE OF INVENTION: Sys NUMBER OF SEQUENCES: 61 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-434-831B-1/C
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US-08-582-776C-1
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QQ

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Gaps

Gaps

RESULT 7

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APPLICANT: Stitz, Lothar
APPLICANT: Stoneemann, Anette
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: Dispansetics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
TITLE OF INVENTION: System Diseases
AUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Patent No. 6057094

GENERAL INPORMATION:

APPLICANT: de la Torre, Juan C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF SEQUENCES: 65

CORRESPONDENCE: 65

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DAPA:
APPLICATION NUMBER: US/08/369,822C
FILING DATE: 06-JAN-1995
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NATE:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
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Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUCCHILI, MACGARET A. (Ph.D.)
REGISTRATION NUMBER: 39,44
REFERENCE/DOCKET NUMBER: 1279-194XX
TELECOMMUNICATION INFORMATION:
TELEFAN: 213/682-9200
TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACCAGGCGTCTCGTGGGCCACAT 23
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82.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8910 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 10550 NO. 6
CITY: La JOlla
STATE: California
COUNTRY: United Sta
                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 90017-2571
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US-08-779-764A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE:
US-08-369-822C-19
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                                                              Sequence 1, Aplication US/08892880
Patent No. 544247
GENERAL INFORMATION:
APPLICANT: GENYE, REINER L.
APPLICANT: GENYE, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INFORTON: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENTING SISTEM: PC-DUS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEPFE, EAC K
REGISTRAFE, EAC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELEPHONE: 20371-2600
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                     STREET: 1100 NEW YORK AVENUE, NW, STATE: DC CTTY: WASHINGTON STATE: DC COUNTY: USA ZIP: 2005-3934
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE COMPUTER: IBM PC COMPALIBLE COMPUTER: IBM PC COMPALIBLE COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-369-822C-19/C
; Sequence 19, Application US/08369822C
; Pattent No. 6015660
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipkin, W. I.
Briese, Thomas
Kliche, Stefanie
Schneider, Patrick A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 ACCAGGAGCCTCGTGGTCCAGAT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.28;
82.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
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154..1056
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91..153
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LOCATION:
                                                US-08-892-880-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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; LOCATION;
US-08-892-880-1
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Borna Disease Viral Sequences,
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                            Length 8910;
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                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREEF: 865 South Figueroa Street, 29th Floor
TITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER RADDABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT 8.0
SOFTWARE: ASCII (DOS) TEXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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Pred. No. 37;
                                                                                                                                                                                                            Score 16.6;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,822
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A. (Ph.D.)
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194C1
TELECOMMUNICATION INFORMATION:
TELEFAX: 213/892-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08434831B Patent No. 6113905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kliche, Stefanie
PSPLICANT: Schneider, Patrick A.
APPLICANT: Stitz, Loth Patrick A.
APPLICANT: Schneemann, Anette
                                                                                                                                                                                                                                                                                            1 ACCAGGCGTCTCGTGGGCCACAT 23
                                                                                                                                                                                                                                                                                                                    76 ACCAGGCGTCTCTTGGGTGCCAT 54
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82.6%;
                                                                                                                                                                                                            72.2%;
82.6%;
                 LENGTH: 8910 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
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                                                                                                                                                                                               Query Match
Best Local Similarity 82.69
Matches 19; Conservative
    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lipkin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90017-2571
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                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-434-831B-19/C
                                                                                                                                                ; ANTI-SENSE:
US-08-582-776C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-434-831B-19
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COUNTRY:
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APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Striche, Stefanie
APPLICANT: Schneider.
APPLICANT: Schneemann, Parrick A.
APPLICANT: Schneemann, Anette
APPLICANT: Schneemann, Anette
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 8910;
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                                                                                                                                                                                                                                                                                                                                                                                           72.2%; Score 16.6; I 82.6%; Pred. No. 37; Live 0; Mismatches
               ATTORNEY AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2837
FELEPHONE: (619) 784-2939
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8910 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,776C
FILING DATE: 04-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/369,822
FILING DATE: 05-JAN-1995
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,831
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A.
REGISTRATION NUMBER: 39,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 1279-194C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08582776C
Patent No. 6077510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 ACCAGGCGTCTTTGGGTGCAT 54
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCAGGCGTCTCGTGGGCCACAT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 213/892-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.2
Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                    linear
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE: NO
US-08-779-764A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-582-776C-19/c
                                                                                                                                                                                                                                                                       TOPOLOGY:
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NUMBER OF SEQUENCES: 27
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ORGANISM: Homo sapiens
                                                                                                                                                         LENGTH: 3157
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US-09-232-200-58
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US-09-285-601-3
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                                                                                                                            SEQ ID NO:3
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                                                                                                                                                                                                                                                                                                                                                                                                              Improved methods for transforming Phaffia and recombinant DNA for use therein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 31

CORRESPONDENCES: 31

CORRESPONDENCES: 31

CORRESPONDENCES: 31

CORRESPONDENCES: 31

COUNTY: Washington

STATE: 1000

COUNTY: United States of America

CONFORTY: United States of America

ZIP: 20006-1888

COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC computeR

COMPUTER: IBM PC compatible

COMPUTER: IBM PC computeR

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   0; Mismatches
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85.7%; Pred. No. 51;
iive 0; Mismatches
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; LOCATION: 18.443
; OTHER INFORMATION: /product= "PRCDNA95"
US-09-091-725-50
                                                                                                                                                                                                                                                                                  Sequence 50, Application US/09091725 Patent No. 6329141
                                                              1 ACCAGGCGTCTCGTGGGCCACAT 23
                                                                                                                     76 ACCAGGCGTCTCTTGGGTGGCAT 54
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ANTI-SENSE: NO
ORIGIRAL SOURCE:
ORGANISM: Phaffia rhodozyma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CCAGGCGTCTCGTGGGCCACA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Patent No. 5198347
                                                                                                                                                                                                                                                 US-09-091-725-50/C
                                                                                                                                                                                                                       RESULT 12
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Gaps
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Fatent No. 6246128
GENERAL INFORMATION:
APPLICANT: Chen, Hong
APPLICANT: Chether, Welson
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
FILE REFERRENCE: 7853-7089
CURRENT APPLICATION NUMBER: US/09/285,601
CURRENT FILING DATE: 1999-04-02
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 6709
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GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Barvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MB
CURRENT APPLICATION NUMBER: US/09/232,200A
FILER REFERENCE: WH197-21p3MB
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FESSEQ for Windows Version 3.0
SEQ ID NO 58
LENGTH: 3098
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                  70.4%; Score 16.2; 185.7%; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.4%; Score 16.2;
85.7%; Pred. No. 56;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,837
FILING DATE: 20-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 58, Application US/09232200A
; Patent No. 6288213
                                                                                                                                                                                                                                                                                           DD 1248 CAGGGTCACTTGGGCCACAT 1268
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                                                                                                                                                           Query Match
Best Local Similarity 85.7'
Matches 18; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
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Sequence 708, Application US/09060756

Fatent No. 6183957

GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gradon, Stephen
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gradon, Stephen
APPLICANT: Gradon, Stephen
APPLICANT: Alain
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOUTHARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : LOCATION: (various positions within the sequence)
: OTHER INFORMATION: applicants are uncertain of bases designated as "n" US-09-060-756-708
                                                                                                Length 3098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 175;
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APPLICANT: MacCollin, Mia M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.6; DE
Pred. No. 92;
0; Mismatches
                                                                                                                                             Mismatches
                                                                                                                   83;
                                                                                              Score 15.8;
Pred. No. 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 116, Application US/08171718 Patent No. 5707863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CCAGGCGTCTCGTGGGCCACAT 23
                                                                                                                                                                                                              Db 1417 GGCTTCTCGTGGGCCAGAT 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.8%;
Best Local Similarity 81.8%;
Matches 18; Conservative
                                                                                           Query Match 68.7%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                     5 GGCGTCTCGTGGGCCACAT 23
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                         ; ORGANISM: Rattus norvegicus US-09-232-201-58
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21P: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy A:-
COMPUTER: IRW TOPERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        804-954-090-60-SD
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                                                                      DB 4; Length 3098;
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                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Marvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Tartaglia, Louis A.
TILLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-Z1p3M.
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
SOFTWARE: FastSEQ for Windows Version 3.0
SOTUMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8; DE
Pred. No. 83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
EARLIER PELING DATE: 1998-01-15
EARLIER PELING DATE: 1998-02-20
EARLIER PELING DATE: 1998-12-04
NUMBER: OF SEQ ID NOS: 105
SEQ ID NO: 58
                                                                    Score 15.8; D
Pred. No. 83;
0; Mismatches
                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09232197A Patent No. 6300096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/09232201A Patent No. 6348321
                                                                                                                                                                                  1417 GGCTTCTCGTGGGCCAGAT 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.78;
                                                                 Query Match 68.7%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                           5 GGCGTCTCGTGGGCCACAT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-232-197-58
; ORGANISM: Rattus norvegicus US-09-232-200-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.7
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            US-09-232-197-58
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Gaps

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Sequence 1, Application US/08160524A

Patent No. 5851761
GENERAL INFORMATION:
APPLICANT: McAdam, Ruth Anne
APPLICANT: Zalnuddin, Zalnul Fadziruddin B.
APPLICANT: Catty, David
TITLE OF INVENTION: DFTECTION AND DIFFERENTIATION OF MYOCBACTERIA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEMP PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEMP PC COMPATIBLE
COMPUTER: Patentin Release #1.0, version #1.25
SOFTWARE: Patentin Release #1.0, version #1.25
CURSTRICATION NUMBER: US/08/160,524A
FILING DATE: 01-DEC-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/752,661
FILING DATE: 18-CT-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9000411.0
FILING DATE: 09-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FEB-1990
PRIOR APPLICATION NUMBER: CB 9000411.0
FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFOWATION:
ANAME: 12-FEB-1990
ATTORNEY/AGENT INFOWATION:
ANAME: NAME: 07-FEB-1990
ATTORNEY/AGENT INFOWATION:
ANAME: NAME: 07-FEB-1990
                                              NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   67.8%; Score 15.6; 181.8%; Pred. No. 94;
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REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-55387-1/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 ACCAAGCAGCTTGTGGGCCACA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACCAGGCGTCTCGTGGGCCACA 22
FILING DATE: 04-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.8°
Best Local Similarity 81.8°
Matches 18; Conservative
                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                      both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 21
US-08-160-524A-1/C
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US-08-478-087-116
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US-08-478-087-116
Sequence 116, Application US/08478087
Patent No. 6077685
APPLICANT: Trofatter, James A. APPLICANT: WacCollin, Mia M. APPLICANT: Gusella, James F. TITLE OF INVEWTION: Tumor Supressor Gene Merlin and Uses; TITLE OF INVEWTION: Thereof, NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS: 320
ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.8%; Score 15.6; DB 1; Length 335; 81.8%; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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ZIP: 20005-3934

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,087
FILING DATE: 07-JUN-1995
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US 08/171,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-EE-1993
PRIOR APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FE-1993
PRIOR APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FE-1993
PRIOR APPLICATION NUMBER: US 08/025,034
FILING DATE: US 08/025,034
                                                                     PRIOR PAPLICATION DATA:
PRIOR PELICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEX/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36.463
REGISTRATION NUMBER: 0609.3850003
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
TELEPROX. (202) 371-2540
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
     APPLICATION NUMBER: US/08/171,718 FILING DATE: 22-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.8
Matches 18; Conservative
                                                   CLASSIFICATION: 436
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US-08-171-718-116
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Gaps

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); DB 4; Length 1938;
1e+02;
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                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
JEDRICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Cahl, Andreas
APPLICANT: Cahlsh, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
ITILE OF INVENTION: EATITY ACID TRANSPORT PROTEINS
FILE REPERENCE: WH197-21p3MC
CURRENT FILING DATE: 1999-01-14
EARLIER PELICATION NUMBER: 60/091,491
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/011,374
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-10-04
SACIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 105
SCOTWARE: FastSEQ for Windows Version 3.0
FROMEWORLD 1998
                                                                                                                                                                                                                                                                                            Score 15.6; DB 4;
Pred. No. 1e+02;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.8%; Score 15.6; D
81.8%; Pred. No. 1e+0
:ive 0; Mismatches
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/09232201A
Patent No. 6348321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08982785A Patent No. 6258929
GENERAL INFORMATION:
APPLICANT: Zhou, Jianhua
                                                                                                                                                                                                                                                                                                                                                                                                          1340 CCGGCCTTCTCGTGGGCCAGAT 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1340 CCGGCCTTCTCGTGGCCCAGAT 1361
                                                                                                                                                                                                                                                                                                                                     0;
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                 2 CCAGGCGTCTCGTGGGCCACAT
                                                                                                                                                                                                                                                                                          Query Match 67.8°
Best Local Similarity 81.8°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Mus musculus
US-09-232-197-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; GENERAL INFORMATION:
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US-08-982-785A-1/c
                                                                                                                                                                                  LENGTH: 1938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-232-201-29
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Pred. No. 1e+02;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.8%; Score 15.6; DB 4; Length 1938; 81.8%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Gimeno, Bavid J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERENCE: WH197-21pJMB
CURRENT FILING DATE: 1999-01-14
EARLIER PPLICATION NUMBER: 60/003, 491
EARLIER APPLICATION NUMBER: 60/003, 491
EARLIER APPLICATION NUMBER: 60/003, 491
EARLIER APPLICATION NUMBER: 60/010, 941
EARLIER PILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
SAFIWARE: FastSEQ for Windows Version 3.0
SQFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/09232197A

Patent No. 6300096

GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3NA
CURRENT APPLICATION UNMER: US/09/232,197A
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT APPLICATION NUMBER: 60/071,374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/09232200A Patent No. 6288213
                                                                                                                                                                                                                                                                                                                                                                                 1271 CGAGGTGGCTCGTCGGCCACAT 1250
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                                                                                                                                                                                                                                                                     67.8%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                       2 CCAGGCGTCTCGTGGGCCACAT
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15 SEQUENCE CHARACTERISTICS:
LENGTH: 1559 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                Query Match 67.8
Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 81.8
Matches 18; Conservative
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                                                                                                                                                                                                  1..853
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                                                                                       TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lir
FEATURE:
                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-08-160-524A-1
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Gaps

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Query Match 67.8%; Score 15.6; DB 4; Length 2983; Best Local Similarity 81.8%; Pred. No. 1e+02; Matches 18; Conservative 0; Mismatches 4; Indels 0;
STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastEGG for Windows 95
SOFTWARE: FastEGG for Windows Version 2.0b
FILICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/031,556
FILING DATE: D0-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 05311/018001
TELEFONENICATION INFORMATION:
TELEFONENICATION TO SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2983 DASSE PARIES
TYPE: NUCLE TYPE: CDNA
FEATURE:
NOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: COGING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: Coding Sequence
; LOCATION: 366...2633
US-08-982-785A-1
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Search completed: December 2, 2002, 21:03:29 Job time : 54 secs 163 ACCAGGCGCTTGGTGGGCGACA 142 g

1 ACCAGGCGTCTCGTGGGCCACA 22

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Gaps

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Sequence 97, Appl Sequence 22850, A Sequence 249, App Sequence 200, App Sequence 200, App Sequence 849, App Sequence 849, App Sequence 849, App Sequence 1615, App Sequence 555, App Sequence 556, App Sequence 554, App Sequence 904, App Sequence 902, App Sequence 902, App
                                                                                                  (without alignments)
164.031 Million cell updates/sec
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                                                                                2, 2002, 21:02:48; Search time 54 Seconds
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2: /cgnz_6/ptodata/2/pubpna/PCT_NEW_PUB_seq:*
3: /cgnz_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgnz_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgnz_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgnz_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgnz_6/ptodata/2/pubpna/NS08_NEW_PUB.seq:*
8: /cgnz_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgnz_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
10: /cgnz_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgnz_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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13: /cgnz_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgnz_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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0 US-09-864-761-25850
0 US-09-974-300-249
0 US-09-905-291A-200
0 US-09-903-230-200
0 US-09-909-0885-200
0 US-09-909-0887-2
0 US-09-833-381-849
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0 US-09-834-1615
10 US-09-764-847-1615
10 US-09-764-87-1615
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10 US-09-764-853-904
10 US-09-764-853-904
10 US-09-764-853-904
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                                                                                                                                                                                                                                           341543 seqs, 192557720 residues
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                                                                                                                                                                      1 accaggcgtctcgtgggccacat 23
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Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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seq length: 200000000
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Match Length DB
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117.22
117.22
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Gaps

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Length 10432;

100.0%; Score 23; DB 10; Length 1 100.0%; Pred. No. 0.031; ive 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 23; Conservative

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Sequence 25850, Application US/09864761 Patent No. US20020048763A1

US-09-864-761-25850

RESULT 2

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng

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; NAME/KEX: misc_feature ; OTHER INFORMATION: Incyte ID No. US20020119463A1 2700132CB1 US-09-919-172-97

TYPE: DNA ORGANISM: Homo sapiens

FEATURE:

				132		NET	
			T Contra	571	٠.	SEO ID NO	
			S: 102	SEQ ID NOS: 102	NUMBER OF SE	NUMBI	
		-28	PRIOR FILING DATE: 2000-07-28	: DATE:	R FILING	; PRIO	
	222,469	60/2	UMBER:	ATION N	R APPLIC	PRIO	
	CURRENT APPLICATION NUMBER: US/09/919,172	: US	CURRENT APPLICATION NUMBER: US/0	ICATION	ENT APPI	; CURRI	
			0036 US	ICE: PA-	FILE REFERENCE: PA-0036 US	; FILE	
	CANCER MARKERS	Ţ, C	PROSTA	ENTION:	TITLE OF INVENTION:	; TITL	
	Turner, Christopher M.	əydc	Christ	Turner,	APPLICANT: Turner, Ch	, APPL	
			arv	Paris, M	ICANT: F	APPL	
			7403A1	TTOZOOZO	FALERIC NO. USZUGZUI.	. GENER	
	919172	560/	; Sequence 97, Application US/09919172	Applica	nce 97,	Seque	
				2/10	1 19-172-9	RESULT US-09-9	
	ALIGNMENTS						
	822-	10	2296	65.2	15	4	
e 261,	S-09-962-436-26	10	1685	65.2	15	4	
Sequence 133, App	US-U9-954-531-133	ם ת	1605	65.2	J L	4 4	
	Ď į	10	1120	65.2	15	4 -	
38,	Б	10	1094	65.2	15	4	
Sequence 31, Appl Sequence 32, Appl	US-09-737-149-31 US-09-737-149-32	10	1083	65.2	15	ח ייי	
Sequence 7076, Ap	5	10	553	65.2	15	c 37	
Sequence 338, App	US-09-764-887-338	10	32190	66.1	15.2	æ	
Sequence 50', APP Sequence 63, Appl	US-10-044-090-63	175	4465	66.1	15.2	35	
Sequence 29, Appl	US-09-801-574-29	10	2120	66.1	15.2	m r	
Sequence 209, App	US-10-040-739-209	σ	517	66.1	വ	m	
	US-09-349-015-8	10	3111	67.0	າທ	'n	
Sequence 190, App	US-09-764-853-190	10	2858	67.0	15.4	.7 ~	
	US-09-908-711-18	10	2858	67.0	വ	7	
	US-09-764-853-378	10	1702	67.0	ഗ	(7)	
Sequence 5554, Appl	US-09-813-242-3534 US-09-908-711-64	20	1702	67.0	15.4	4 (
	US-09-974-300-4778	10	921	20.7	Ωu	C 24	
6316	US-09-864-761-631	10	476	67.8	15.6	23	
2116	US-09-864-761-211	10	475	67.8	S	c 22	
equence 1122	09-815-343-1122	10	345	67.8	15.6	1 (1	
	001-136-130-00-	5	306	0 63	זה	000	

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APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica *X -1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2010-105-23
PRIOR PAPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.4
INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.2
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.8
INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.9
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SEQ ID NO 9296
LENGTH: 573
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Pred. No. 16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR PLICATION NUMBER: US 60/207,456
PRIOR PLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2011-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-31
PRIOR PILING DATE: 2000-09-30
PRIOR PILING DATE: 2000-09-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2001-01-39
PRIOR FILING DATE: 2001-01-39
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PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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Application US/09864761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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86.4%;
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Best Local Similarity
Matches 19; Conserv
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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86.4%; Pred. No. 15;
Live 0; Mismatches 3; Indels C
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N: EXPRESSED IN BARLIN, SIGNAL = 3.4
N: EXPRESSED IN PLACENTA, SIGNAL = 4.2
N: EXPRESSED IN BONE MARROW, SIGNAL = 5.8
N: EXPRESSED IN LUNG, SIGNAL = 2.3
N: EXPRESSED IN LUNG, SIGNAL = 4.9
N: EXPRESSED IN HERT, SIGNAL = 4.7
N: EXPRESSED IN HELA, SIGNAL = 3.4
N: EXPRESSED IN HELA, SIGNAL = 3.4
N: WITH 11: 916677847, EVALUE 4.40e-01
N: EST HUMAN HIT: AI580035.1, EVALUE 2.60e+00
N: SWISSPROT HIT: Q64411, EVALUE 1.00e+00
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                                                                                                                                        PRIOR PELLING DATE: 2001-03-23
PRIOR FILLING DATE: 2000-02-04
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELLOGATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-36
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-09-07
PRIOR PELLING DATE: 2000-09-37
PRIOR PELLING DATE: 2000-09-37
PRIOR PELLING DATE: 2001-01-30
                                                     FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-06-
PRIOR APPLICATION NUMBER: U
PRIOR FILING DATE: 2001-01-
NUMBER OF SEQ ID NOS: 49117
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Best Local Similarity 86.4
Matches 19; Conservative
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US-09-864-761-25850
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SEQ ID NO 25850
LENGTH: 189
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267 ACCATGGGTCACGTGGGCCACA 288

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RESULT 3 US-09-864-761-9296

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Score 16.6; DB
Pred. No. 31;
0; Mismatches
             PRIOR FILING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PLILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-09-08
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PPLICATION NUMBER: PCT/US99/20594
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-16
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PRIOR FILING DATE: 2000-01-05
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; Patent No. US20020132240A1
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Grimaldi, Christopher J.
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82.6%;
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Filvaroff, Ellen
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FILING DATE: 1999-07-07
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Mather, Jennie P.
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Botstein, David
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Best Local Similarity 82.6
Matches 19; Conservative
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Gao, Wei-Qiang
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SEQ ID NO 200
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US-09-905-291A-200
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US-09-909-320-200/c
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                Sequence 249, Application US/09974300
Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka. Randy M.
APPLICANT: Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 00/279,526
PRIOR APPLICATION NUMBER: 00/279,526
PRIOR PLING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 249
LENTH: 1557
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Best Local Similarity 90.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-249
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Gerber, Hanspeter
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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                                                                   -09-974-300-249/c
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DB 9; Length 2372; Indels

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APPLICANT: SERVAIL, TIMOCHY A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, P. Mitckey
APPLICANT: Wood, Williams, P. Mitckey
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-11
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 1046-11
FILING DATE: 2001-07-18
CURRENT FILING DATE: 2001-07-18
FRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: PCT/US99/2054
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2064
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/2069
PRIOR FILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PRIOR PRILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PRILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PRILING DATE: 1999-11-20
PRIOR PRILI
                                                           Godowski, Paul J.
Grimaldi, Christopher J.
                                                                                                     Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
                       Gerritsen, Mary E.
                                                                                                                                                                                                      Paoni, Nicholas F.
  Gerber, Hanspeter
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APPLICANT:
APPLICANT:
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82.6%; Pred. No. 31;
Live 0; Mismatches
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Stewart, Timothy A.
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Best Local Similarity
Matches 19; Conserv
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US-09-909-088B-200/c
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RESULT 8 US-10-006-867-5/c

Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang

Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L.

APPLICANT:
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APPLICANT:

1998-08-1

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R APPLICATION NUMBER: 60/101475
R FILING DATE: 1998-09-23
R FILING DATE: 1998-09-24
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/101743
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/101916
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/102570
R APPLICATION NUMBER: 60/102570
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R APPLICATION NUMBER: 60/103570
R FILING DATE: 1998-09-30
R APPLICATION NUMBER: 60/103679
R FILING DATE: 1998-09-30
                                                                           R APPLICATION NUMBER: 60/097971
R FILING DATE: 1998-08-26
R FILING DATE: 1998-08-26
R RPLING DATE: 1998-08-26
R APPLICATION NUMBER: 60/098749
R FILING DATE: 1998-09-01
R RPLICATION NUMBER: 60/099741
R FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/100662
FILING DATE: 1998-09-16
FILING DATE: 1998-09-16
FILING DATE: 1998-09-17
FILING DATE: 1998-09-17
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                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/099763
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099792
FILING DATE: 1998-09-10
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/100930
FILING DATE: 1998-09-17
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APPLICATION NUMBER: 60/106030
FILING DATE: 1998-10-28
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FILING DAFE: 1998-10-30
APPLICATION NUMBER: 60/106856
FILING DATE: 1998-11-03
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FILING DATE: 1998-11-17
APPLICATION NUMBER: 60/112419
FILING DATE: 1998-12-15
    APPLICATION NUMBER: 60/096959
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/099812
FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/099815
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FILING DATE: 1998-09-22
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FILING DATE: 1998-10-08
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FILING DATE: 1998-10-08
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APPLICATION NUMBER: 60/113011
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APPLICATION NUMBER: 60/112854
                                                           ILING DATE: 1998-08-26
    A PELICANI MATERIA CALI M. A.
TITLE OR INVENTION MATERIA COLI MATERIA CALI M. A.
TITLE OR INVENTION MATERIA COLI MATERIA CALI M. A.
TITLE OR INVENTION MATERIA COLI MATERIA CALI MATERIA
                                                                                                                                    Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Watanabe, Colin K.
Wood, William I.
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FILING DATE: 1998-08-17
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FILING DATE: 1998-08-18
, Application US/10006867
US20020119130A1
                                                                             Filvaroff, Ellen
Gerritsen, Mary E.
                    Patent No. US2002011
GENERAL INFORMATION:
APPLICANT: Eaton, Da
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APPLICANT:
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1998-12-15

Gaps

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US-09-833-381-853/c

US-09-833-381-853/c

Sequence 853, Application US/09833381

Patent No. US20020132090A1

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs

TITLE OF INVENTION: No. US20020132090A1e1 Nucleic Acid and Protein Homologs

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2000-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 853

LENTH: 2404
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APPLICANT: HORDER DATE:
APPLICANT: Workley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-w0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN WORS: 3950
SEQ ID NO 3049
LENGTH: 339
                                                                                                                                                                                                                                                                                                    Length 2404;
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Pred. No. 31;
0; Mismatches
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Pred. No. 31
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 2404
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; Patent No. US20020142981A1
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82.68;
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Best Local Similarity 82.6%;
Matches 19; Conservative
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Best Local Similarity 82.0.
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; ORGANISM: Homo sapiens
US-09-833-381-853
                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-833-381-849
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ORGANISM: Homo sapiens
FEATURE:
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US-09-880-107-3049
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Best Local Similarity 82.6%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches
                      PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR PELICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR PELING DATE: 1998-12-23
PRIOR PELING DATE: 1998-12-23
PRIOR PELING DATE: 1998-12-33
PRIOR PELING DATE: 1999-10-12
PRIOR PELING DATE: 1999-10-12
PRIOR PELING DATE: 1999-10-12
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-12
PRIOR PELING DATE: 1999-01-20
PRIOR PELING DATE: 1999-02-19
PRIOR PELING DATE: 1999-02-19
PRIOR PELING DATE: 1999-02-10
PRIOR PELING DATE: 1999-02-11
PRIOR PELING DATE: 1999-02-11
PRIOR PELING DATE: 1999-02-11
PRIOR PELING DATE: 1999-04-13
PRIOR PELING DATE: 1999-04-15
PRIOR PELING DATE: 1999-04-16
PRIOR PELING DATE: 1999-04-16
PRIOR PELING DATE: 1999-04-17
PRIOR PELING DATE: 1999-06-19
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; Patent No. US20020132090A1
; GENERAL INFORMATION:
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221 ACCAGGAGCCTCGTGGTCCAGAT 199
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Conservative
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US-09-764-870-555
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Best Local Similarity
Matches 16; Conserv
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Matches 16; Conserv
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US-09-764-870-556/c
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US-09-764-870-556
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US-09-764-853-903
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Sequence 1615, Application US/09764847

Sequence 1615, Application US/002032767A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies

FILE REFERENCE: PC009

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 2003

SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: LOGICIA CONTRACT C
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 T10108 US-09-880-107-3049
                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INFORMATION:
FILE REFERENCE: PC009
CURRENT FILING DATE: 2001-01-17
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 2003
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1616
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                                                                                                Score 16.4; DB 10;
Pred. No. 37;
0; Mismatches 1;
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Pred. No. 50;
0; Mismatches
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85.7%; Pred. No. 50;
cive 0; Mismatches
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Patent No. US20020042386A1
GENERAL INFORMATION:
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85.7%;
                                                                                                Query Match 71.3%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                      322 GGCGTCTCGTGGGCCAAA 339
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ORGANISM: Homo sapiens
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US-09-764-847-1616/c
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US-09-764-870-555
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Pred. No. 62;
0; Mismatches 0; Indels 0;
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Patent No. US20020090672A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06

CURRENT APPLICATION NUMBER: US/09/764,853

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 939

SEQ ID NO 903
                                                CURRENT PAPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 555
LENGTH: 10957
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
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100.0%; Pred. No.
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100.08; Fr.
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100.08; Pic
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Best Local Similarity 100.
Matches 16; Conservative
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TYPE: DNA ORGANISM: Homo sapiens
                                                TYPE: DNA
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Sequence 554, Application US/09764870

Sequence 554, Application US/09764870

SERERAL INFORMATION:

TILLE OF INVENTION:

TILLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 554

LENGTH: 13220
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62;
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Sequence 902, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ206
CURRENT APPLICATION NUBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
                                                                                                                     Sequence 904, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT FILING DATE: 2001-01-17
PRIOR application data removed - consult PALM or file wrapper
UNDER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
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                     5005 GTCTCGTGGGCCACAT 4990
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Matches 16; Conservative
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8 GTCTCGTGGGCCACAT 23
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CRGANISM: Homo sapiens
US-09-764-870-554
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CORGANISM: Homo sapiens
US-09-764-853-904
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Best Local Similarity
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US-09-764-853-902
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US-09-764-870-554
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US-09-764-853-904
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Howelver, David R.
APPLICANT: Howelver, David R.
TITLE OF INVENTION: EURE EXPRESSION ANALYSIS BY MICROARRAY
FILLS OF INVENTION: EURE EXPRESSION ANALYSIS BY MICROARRAY
FILLS OF INVENTION: EURE EXPRESSION ANALYSIS BY MICROARRAY
FILLS OF INVENTION: EUG. E. 201.05-23.
FILLS REPRENCE: AGOING A.
CURRENT FILLNE DAVE: 2000-02-04
FRIOR FILLNE DAVE: 2000-02-04
FRIOR FILLNE DAVE: 2000-03-04
FRIOR FILLNE DAVE: 2000-03-04
FRIOR FILLNE DAVE: 2000-03-07
FRIOR FILLNE DAVE: 2000-03-07
FRIOR FILLNE DAVE: 2000-03-07
FRIOR FILLNE DAVE: 2001-01-30
FRIOR FILLNE DAVE: 2001-01-30
FRIOR FILLNE DAVE: 2001-01-30
FRIOR FILLNE DAVE: 2001-01-30
FRIOR PAPLICATION NUMBER: PCT/USO1/0066
FRIOR FILLNE DAVE: 2001-01-30
FRIOR PAPLICATION NUMBER: PCT/USO1/0066
FRIOR FILLNE DAVE: 2001-01-30
FRIOR PAPLICATION NUMBER: PCT/USO1/0066
FRIOR FILLNE DAVE: 2001-01-30
FRIOR FILLNE DAVE: 2
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62;
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100.0%; Pred. No. v...
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PRIOR FILLING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8210 GTCTCGTGGGCCACAT 8225
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 902
LENGTH: 13220
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                               , ORGANISM: Homo sapiens
US-09-764-853-902
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US-09-864-761-18859/c
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Sequence 6316, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO:
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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N: EXPRESSED IN ADULT LIYER, SIGNAL = 2.6
N: EXPRESSED IN BT474, SIGNAL = 3.1
N: EXPRESSED IN PLACENTA, SIGNAL = 3.2
N: EXPRESSED IN PLACENTA, SIGNAL = 2.5
N: EXPRESSED IN HELA, SIGNAL = 2.4
N: EXPRESSED IN HELA, SIGNAL = 3.9
N: EXPRESSED IN HEART, SIGNAL = 3.9
N: EXPRESSED IN BOWE MARROW, SIGNAL = 3.1
N: EXPRESSED IN BOWE MARROW, SIGNAL = 2.1
N: EXPRESSED IN BRAIN, SIGNAL = 2.1
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                                                                                       PRIOR FILING DATE: 2000-10-4
PRIOR PPLICATION NUMBER: GB 24263.6
PRIOR PRILING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-31
PRIOR PLING DATE: 2000-09-30
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Pred. No. 89
                                                                  FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
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81.8%;
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP T
OTHER INFORMATION: EXPRE
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Best Local Similarity
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US-09-864-761-6316
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine
APPLICANT: Xi, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: Xing, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121:504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH::345
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                                                                                                                                                                                                                                                                                                                                                                   EXPRESSED IN BRAIN, SIGNAL - 2
NT HIT: Y13614.1, EVALUE 7.40e-01
SMISSPROT HIT: P50061, EVALUE 1.90e+00
EST_HUMAN HIT: A1817915.1, EVALUE 1.10e+00
                                                                                              N: EXPRESSED IN BT474, SIGNAL = 1
N: EXPRESSED IN FFFAL LIVER, SIGNAL = 3.2
N: EXPRESSED IN PLACENTA, SIGNAL = 3.3
N: EXPRESSED IN HELLO, SIGNAL = 25
N: EXPRESSED IN HELA, SIGNAL = 2.4
N: EXPRESSED IN HEART, SIGNAL = 3.9
N: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
N: EXPRESSED IN LONG, SIGNAL = 2.1
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                                                                  ADULT LIVER, SIGNAL = 2.6
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Pred. No. 88;
0; Mismatches
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Pred. No. 89;
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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81.8%;
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Best Local Similarity 81.8%;
Matches 18; Conservative
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Best Local Similarity 81.8
Matches 18; Conservative
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ORGANISM: Homo sapien
                        OTHER INFORMATION: MACHER INFORMATION: ED: OTHER INFORMATION: ED: OT
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US-09-864-761-2116/c
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FEATURE:
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APPLICANT: Yammoto, Robert T.
APPLICANT: Yammoto, Robert T.
TITLE OF INVENTION: Indentification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFREENCE: ELTTRA.011A
CURRENT APPLICATION UNMERR: US/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOCTWARK OF SEX END FOR WINDOWS VERSION 4.0
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression
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Pred. No. 91;
0; Mismatches
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                   TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US CORRENT APPLICATION NUMBER: US/09/974,300 CURRENT APPLICATION NUMBER: US/09/976,300 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR PILING DATE: 2001-006 PRIOR PILING DATE: 2001-03-27 NUMBER OF SED ID NOS: 8481 SOFTWARE FESSESE FOR Windows Version 4.0 SEQ ID NO 4778
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Patent No. US20020061569A1
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81.8%;
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
Trawick, John D.
APPLICANT: Carr, Grant J.
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Best Local Similarity 81.8%;
Matches 18; Conservative
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US-09-974-300-4778
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Best Local Similarity 81.8
Matches 18; Conservative
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LENGTH: 2685
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN HEARY, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN HEARIN, SIGNAL = 8.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.3

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.5

US-09-864-761-6316
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                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-36
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELICATION NUMBER: US 00/236,359
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: US 60/236,359
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PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR PELICATION NUMBER: PCT/US01/00665
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR PELICATION NUMBER: PCT/US01/00670
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PRIOR PELICATION NUMBER: US 09/774,203
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PRIOR PELICATION NUMBER: US 09/774,203
PRIOR PELICATION NUMBER: US 09/774,203
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81.8%; Pred. No. 89;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ACCAAGCAGCTTGTGGGCCACA 170
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Matches 18; Conservative
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US-09-974-300-4778/c
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Indels

Query Match

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Search completed: December 2, 2002, 22:25:33 Job time : 79 secs

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AL229510 Tetraodon

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Ad118418 mp54e07.r
Ad11139 T7 end of
AV625131 AV625131
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BB614523 BB614523
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BC77692 BC77692 BC77692 BC77692 BC77692 BC77692
BC77692 AV113795 AV113795

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Perfect score: Sequence:

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862 bp mRNA linear EST 13-FEB-2001
ALS27673 LTLNFL003_NBC3 Homo sapiens cDNA clone CSODC026YF17 5
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRX cedex - France
Email: seqreféqenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/clone="cs0bc026Fr17"
/clone="ltl_NFL003_NBC3"
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BC281235
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AQ751572
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BG3443568
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BB614523
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AZ427383
BG476962
BG476964
BF101715
BF983345
BE871682
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CNSO4U73
BF844922
BF844924
BE751852
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BF512290
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AV663489
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AL527673/c
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AA355973 EST64454
AA279738 zs92ell.r
AL166419 Tetraodon
BEZ62736 601150609
BM802340 AGENCOURT
                                                                                                   (without alignments)
179.085 Million cell updates/sec
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                                                                                    2, 2002, 20:57:49; Search time 2080 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                           32135990
            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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1 accaggcgtctcgtgggccacat 23
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AA279738
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em_gss_rod:*
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I (bases 1 to 248)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,

O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,

Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald

L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Wedhman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dinke, D., Feng, D.-Fr, Fertle, A., Fischer, C., Hastings, G.A., He, W.W.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Wei, Y.E., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon

W.R., Rosen, C.A., Hassline, W.A., Fields, C., Fraser, C.M. and

Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA355973 248 bp mRNA linear EST 21-APR-1997
EST64454 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
finformation related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                   Length 862;
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 9; 100.0%; Pred. No. 7.2;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ki-67 antigen, mRNA sequence.
AA355973
AA355973.1 GI:2008291
                                                                                                                                                                                                                                                                                                                                                                                             398 ACCAGGCGTCTCGTGGGCCACAT 376
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1 (bases 1 to 127)
NOT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                   AA279738 12-T5-AUG-19 mRNA 11near EST 15-AUG-19 zs92e11.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704972 59 similar to SW:KI67_HUMAN P46013 ANTIGEN KI-67. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@inage.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Insert Length: 1112 Std Error: 0.00
           /cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                           Gaps
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                                                              6 others
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34;
/clone_lib="Jurkat T-cells VI"
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15;
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100.0%; Pred. No. 34;
iive 0; Mismatches
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                                                                                                          Score 22;
Pred. No. 1
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AA279738.1 GI:1921203
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95.7%;
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Matches 22; Conserv
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LOCUS

RESULT 4 CNS01TEI ORGANISM

REFERENCE AUTHORS

REFERENCE AUTHORS

JOURNAL

TITLE

KEYWORDS SOURCE

ACCESSION VERSION

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934 bp mRNA linear EST 05-MAR-2002 5', mRNA sequence. BM802340 I GI:19119163
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.ningov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Can be

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM176 row: b column: 04

High quality sequence start: 54

High quality sequence start: 54

High quality sequence start: 295.
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/tlab.nost="neuroblastoma"
/lab.nost="neuroblastoma"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; cDNA made by ollgo-dT priming. Directionally
cloned into ECORIX/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NTH_MGC Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
Tissue Procurement: ATC
CODM Library Preparation: Life Technologies, Inc.
CDM Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12342 row: a column: 15
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 18.4; DB 10; 95.0%; Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3503139"
/clone_lib="NIH_MGC_19"
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BM802340
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                                                                                                                  CNSOlTEI 954 bp DNA linear GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 194J15 of library G from Tetraodon nigroviridis, genomic survey
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Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcmi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodoniidae; Tetraodon.

I (bases 1 to 954)
Best-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurlin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 625)
NIH-MGC http://mgc.nci.nih.gov/.
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Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the
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/db_xref="taxon:99883"
/clone="194J15"
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Pred. No. 4.8e+02;
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Submitted (12-APR-2000)
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AL166419.1 GI:7804157
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90.9%;
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FEATURES

TITLE JOURNAL

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AUTHORS

JOURNAL REFERENCE

TITLE

BASE COUNT ORIGIN

Matches

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BE262736/c

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        /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                            CNSO3631 107 bp DNA linear GSS 15-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 215111 of library G from Tetraodon nigroviridis, genomic survey
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large facts sequence is a single project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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/db_xref="taxon:99883"
/clone="215111"
                                                                                                                                                      Score 17.8; DB 14;
Pred. No. 1.3e+03;
); Mismatches 2;
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Pred. No. 1.3e+03;
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/clone_lib="G"
/note="Genoscope sequence ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
/clone_lib-"NIH_MGC_67"
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GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                             Technologies.
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90.58;
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Best Local Similarity 90.5%;
Matches 19; Conservative
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note="Vector: pt7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I: - oligo(dT) primer [5/ Parand class primed with a Not I: - oligo(dT) primer [5/ Parand class primed with Not I and cloned into the Not I and cloned into the Not I and cloned into the Not I and Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified ppT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bonaido."
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Yarrowia lipolytica.

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.

E (bases 1 to 1122)

Souciet.J.L., Aigle,M., Artiguenave,F., Blandin,G.,

Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,

Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekkla,F., Toffano.Nioche,C., Wesolowski-Louvel,M.,

Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

L FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNSO6R1T 1122 bp DNA linear GSS 05-JUL-2001 T7 end of clone AWOAA010G07 of library AWOAA from strain CLIB 89 of Yarrowia lipolytica, genomic survey sequence.
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Casargolas, N. Neuveglise, C., Lepingle, A., Bon, E., Feynerol, C.,
Artiguenave, F., Winoker, P. and Gaillardin, C.
Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:347708
Seq primer: -28M13 rev2 from Amersham
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Pred. No. 1.7e+03;
0; Mismatches 1;
                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:573060"
/clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                              /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                 /sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                              High quality sequence stop: 469
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.7%; Scor
94.7%; Pred
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Marray.M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Mooris,M., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2136 row: F column: 16
Seq primer: M13 Reverse
Class: BAC ends
                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="Plate=2136 Col=16 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 522.
Location/Qualifiers
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/hote="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"
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                                                                                                                                                                                                                                                                                                   AV624388 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii 5% to sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu(ekazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Sukaryota i Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 636)
                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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(bases 1 to 511)

Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtil

DNA Res. 7 (5), 305-307 (2000)
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/organism="Chlamydomonas reinhardti1"
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                                                                    Score 17.2;
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/db_xref="taxon:3055"
/clone="LC077b01_r"
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzil, Zygoasccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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/clone_"LC088c08 r"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dloxide concentration in the bubbling gas was changed from
5% to 0.04%"
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                  484. >783
/484. >7783
/note="similar to Saccharomyces cerevisiae ORF YAL002w [
VPS8 ; vacuolar sorting protein, 134 kD ]"
/evidence=not_experimental
a 308 c 257 g 292 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Chlamydomonas reinharda:
Chlamydomonadacae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadacae; Chlamydomonas.

1 (bases 1 to 489)
Asamiaula.

Nasamiaula.
Na Tabata.
Na Tabata.
Of Tabata.
Of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.7%; Score 17.4; DB 17;
85.7%; Pred. No. 2e+03;
iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                         /organism="Yarrowia lipolytica"
/strain="CLIB 89"
/db_xref="taxon:4952"
/clone="AWOAA010G07"
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/note="and: T7"
<484. .>783
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AV625131.1 GI:10774308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Conservative
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                                                                      COMMENT
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SOURCE

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Gaps ö

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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
151 c 114 g 174 t
                                                                                                                                                                                                                                                              A2878371 696 bp DNA linear GSS 05-MAR-2001
RPCI-23-199L7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-199L7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 696)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
AB., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
Mouse BAC End Sequences from Library RPCI-23
Upublished (1999)
Other_GSSs: RPCI-23-199L7.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact pleater de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
712 131 838 0200
Fax: 301 838 0208
              Indels
           3;
           Mismatches
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/db_xref="taxon:10090"
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/sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                          604 CCATGCGTCTCCTGGGCCTCAT 625
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           ;
0
                                                                2 CCAGGCGTCTCGTGGGCCACAT 23
                                                                                                                                                                                                                                                                                                                                                                             AZ878371.1 GI:13196360
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           19; Conservative
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AZ878371
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                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Oxraninci.P., Shibata,Y., Muramatsu,M., and Hayashizahi,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Asawa,M., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Soqabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, adult male testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/dev_stage="adult"
                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .636
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     AUTHORS
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                                                                                                                                                                                                                                                                           LOCUS A2427383 699 bp DNA linear GSS 03-OCT-200
DEFINITION 1M0209L17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                   Gaps
                                                   ;
0
74.8%; Score 17.2; DB 17; Length 696; 86.4%; Pred. No. 2.2e+03; ive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                    AZ427383
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Score 17.2; DB 10; Length 636; Pred. No. 2.1e+03;

74.8%; 86.4%;

Best Local Similarity

Query Match

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mRNA sequence.
mRNA sequence.
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                                                                                         human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalval (gilfy172114) [abanic All The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG476962 724 bp mRNA linear EST 21-MAR-2001 602522177F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4640730 5',
                                                                                                                                                                                                                                                                                                                                                                                                                               S. 2030 E., SLC, UT
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1212 c 142 g 161 t l others
                                                                                                         Mus musculus Sukaryota, Muziata; Craniata; Vertebrata; Euteleostomi; Butaryota; Metazoa; Chordata; Criurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 699)
10 (bases 1 to 699)
11 (bases 1 to 699)
12 (bann, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Molmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0209L17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 8
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0209 row: L column: 17
clone UUGC1M0209L17 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: plasmid ends
High quality sequence stop: 699.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                     AZ427383
AZ427383.1 GI:10551396
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Best Local Similarity 86.4
Matches 19; Conservative
                                                                                         house mouse.
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Gaps

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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone="IRAGE: 1956612"
// Clone="IRAGE: 1956612"
// Clone="Ib="NIH_MGC_88"
// Issue=_type="duodenal adenocarcinoma, cell line"
// lab_host="DH108 (phage-resistant)"
// note="Organ: small intestine; Vector: pcMV-SPORT6;
// Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
// oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
29 a 247 c 283 g 170 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF983345 929 bp mRNA linear EST 23-JAN-2001 602305223F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4396612 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: ATC
CONA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MG.C. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10095 row: n column: 05
High quality sequence stop: 632.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                Length 921;
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            providing samples: Gilbert Smith, NIH"
                                                                                             Score 17.2; DB 12,
No. 2.3e+03;
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86.4%; Pred. No. 2.3e+03;
tive 0; Mismatches 3;
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0; Mismatches
                                            196 g
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BE871682
BE871682.1 GI:10320458
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                                                                                                                                   74.8%;
86.4%;
                                                                                                                                                             Best Local Similarity 86.4 Matches 19; Conservative
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BF983345
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Best Local Similarity
                                      247 a
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BF983345/c
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TITLE
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BE871682
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                                                                                                                                                                                                                                                                                                       /clone_libe_NIH_MGG_20"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic"
/tisue_type="melan
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11 H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAM9177 row: b column: 14
High quality sequence stop: 624.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.2; DB 12;
Pred. No. 2.2e+03;
0; Mismatches 3;
                                                                                      Plate: LLCM1402 row: k column: 04
High quality sequence stop: 710.
Location/Qualifiers
1. 788
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                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:4639227"
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/clone="IMAGE:3980845"
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86.48;
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BF101715
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BF101715/c
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ORGANISM

SOURCE

AUTHORS TITLE JOURNAL

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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Actinopteryyii; Neopteryyii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopteryyii; Percomorpha; Tetraodontiformes; Tetraodontidae: Tetraodon.

1 (bases 1 to 984)

1 (bases 1 to 984)

1 (bases 1 to 984)

1 Sear-Collius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO4U73 984 bp DNA linear GSS 24-MAY-; Tetraodon nigroviridis genome survey sequence SP6 end of clone 046G12 of library B from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                Length 1201;
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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/db_xref="taxon:99883"
/clone="046G12"
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Pred. No. 2.9e+03;
0; Mismatches 0;
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100.0%; Pre
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86.48;
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Best Local Simi
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbelobacil.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3853379"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/tab_host="DH10B (phage-resistant)"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1101)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9577 row: c column: 12
High quality sequence stop: 630.
Location/Qualifiers
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 120pl)
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                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
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Drosophila melanogaster
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source

FEATURES

BASE COUNT ORIGIN

CNS00ZXC/c DEFINITION

RESULT 22

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ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL

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143 ACCAGGTGTCTCCTGGGCCA
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Job time: 2095 secs
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/organism="taxon:9606"
/db.xref="taxon:9606"
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/dev_stage="Adult"
/note="Organ: head_neck; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency.conditions."
                                                                                                                                                                                            Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases i to 341)

1 bases i to 341)

1 bases i to 341)

1 correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=RC4&t2=RC4-HT0978-21200-021-h0&t13=2000-12-22&t4=1)
Seq primer: puc 18 forward
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                                            EST 13-JAN-2001
                                            BF844922 341 bp mRNA linear EST 13-JAN-200
RC4-HT0978-221200-021-h04 HT0978 Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.8e+03;
0; Mismatches 2; Indels 0
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High quality sequence stop: 340
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Best Local Similarity 90.0%;
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/dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 379)
1 blass Neto. Ito 379)
1 blas Neto. Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baila, G.S., Silmson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V. O'Hare
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-HT0978-221200-021-h08&t3=2000-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence start: 10
High quality sequence stop: 379.
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                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

December 2, 2002, 22:47:00 ; Search time 15857 Seconds (without alignments) 17923.819 Million cell updates/sec	US-09-700-906A-1_COPY_197_9962 ore: 9766
December	02-09-70 9766
Run on:	Title: US-09

918046 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0 Scoring table: Sequence: Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 66 Minimum DB : Maximum DB :

em_htg_inv:* em_htg_other:* em_vi:* em_htg_hum:* em_htg_mus:* em_htg_pln:* em_htg_rod:* gb_om:
gb_bat:*
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

em_htgo_hum:* htgo_mus:*

em_htg_mam:*

em_htg_vrt:*

AX48033 Sequence AR032788 Sequence 129528 Sequence 40 191202 Sequence 40 171710 Cladoborryu 142230 Sequence 43 AX118213 Sequence 43 AX118213 Sequence E22184 Yeast capab Y17098 Cladoborryu AR04094 Sequence E22184 Sequence E22184 Sequence AR041096 Sequence AR041096 Sequence AR041096 Sequence AR041096 Sequence AR063137 Sequence 164788 Sequence 164788 Sequence 164788 Sequence 164788 Sequence 17255 Homo sapien 19655 Homo sapien 19656 Homo sapien 19659 Sequence AX270718 Sequence AX270718 Sequence AX270718 Sequence AX270718 Sequence 106069 Sequence 16 AR135505 Sequence AX381699 Sequence AX009578 Sequence AX48325 Sequence AX483936 Sequence AR081408 Sequence AX026790 Sequence AX159132 Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES AX118213 AX128213 AX209041 E22184 CMY17098 HSEZRING18 I31144 HSU14016 AX133328 AX270718 AX27249 131370 S52152831 AX483325 AX483325 AX483328 AX483328 AX483328 AX18332 AX204486 AX204495 AX483033 AF189407 AR032788 AR03278 129528 191202 CMY17101 AR041096 AR060704 AR0603137 AR117026 164788 AR094674 AR096655 HSU96955 HSU96959 HSU96959 HSU96959 HSU96959 HSU96959 HSU96959 HSU96959 AR135505 AX381699 AX009578 142230 DB Query Match Length 26.2 26.2 25.2 25.2 25.2 Score Result No.

PAT 30-AUG-2001 Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 51) Shinkets,R.A. and Leach,M. Nucleic acids containing single nucleotide polymorphisms and methods of use thereof linear DNA 51 bp Sequence 592 from Patent WO0148245. AX204486 AX204486.1 GI:15394046 human. RESULT 1 AX204486 LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE

ALIGNMENTS

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Homo sapiens
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I (bases 1 to 51).
Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 0148245-A 601 05-JUL-2001;
Curagen Corporation (US)
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Accession number cg43968854"
16 c 12 g 8 t
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Patent: WO 0148245-A 592 05-JUL-2001;
Curagen Corporation (US)
Location/Qualifiers
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/organism="Homo sapiens"
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Soudeyns, H., Champagne, P., Holloway, C.L., Silvestri, G.U.,
Soudeyns, H., Champagne, P., Holloway, C.L., Silvestri, G.U.,
Ringuette, N., Samson, J., Lapointe, N. and Sekaly, R.P.
Direct Submitssion
Submitted (24-SE0-1999) Laboratoire d'immunologie, IRCM, 110 avenue
Des Pins ouest, Montreal, Quebec H2W 1R7, Canada
Location/Qualifiers
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1 (bases 1 to 66)

Soudeyns, H., Champagne, P., Holloway, C.L., Silvestri, G.U.,
Ringuette, N., Samson, J., Lapolnte, N. and Sekaly, R.P.
Transient T cell receptor beta-chain variable region-specific expansions of CD4+ and CD8+ T cells during the early phase of pediatric human immunodeficiency virus infection: characterization J. Infect. Dis. 181 (1), 107-120 (2000)
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/protein_id-"AAF29194.1"
/db_xreff-"GI:6841682"
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Pred. No. 8.2e+05;
0; Mismatches 23;
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/organism="Candida albicans"
/db_xref="taxon:5476"
a 14 c 3 g 40 t
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/db_xref="taxon:9606"
/clone="B2660"
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/gene="TCRBV20s1"
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/organism="Hypomyces odoratus"
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Sequence directed DNA binding molecules compositions and methods
Patent: US 6384208+A 400 07-MAX*-2002;
                                                                                                                                  1 (bases 1 to 50)
Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E. Method of determining DNA sequence preference of a DNA-binding molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 50)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
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Best Local Similarity 75.6%; Pred. No. 9.2e+05;
Matches 31; Conservative 0; Mismatches 10,
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                                                                                                                                                                                            Patent: US 5869241-A 400 09-FEB-1999;
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                                          Sequence 400 from patent US 5869241.
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Best Local Similarity 75.6%;
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Appl. Environ. Microbiol. 65 (2), 606-610 (1999)
Sequence-directed DNA-binding molecules compositions and methods Patent: US 5578444-A 400 26-NOV-1996;
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Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 400 10-MAR-1998;
Location/Qualifiers
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Pred. No. 9.2e+05;
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191202.1 GI:3935672
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Y17101.1 GI:3688265
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Hypomyces odoratus
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JP 1999042090-A/69
16-FEB-1999
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 Best Local Similarity 72.7
Matches 32; Conservative
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Picoult-Newburg, L. and Pohl, M. Genotyping reagants, Rits and methods of use thereof Patent: Wo 0129262-A 3336 26-APR-2001; Orchid BioSciences, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 others
                                                                                                                         Length 61;
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Pred. No. 1e+06;
1; Mismatches 13; Indels
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/fissue_type="mycelium"
1 .61
                                                                                                                     0.3%; Score 25; DB 8; 3
ilarity 64.9%; Pred. No. 9.2e+05;
Conservative 0; Mismatches 20
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Sequence 3336 from Patent WO0129262.
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Sequence 43 from patent US 5629153.
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                                                                   /note="microsatellite"
 /isolate="IMI 26134"
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11 c 16 g
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AX118213.1 GI:14035164
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Best Local Similarity 69.6%;
Matches 32; Conservative
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1 (bases 1 to 50)
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60 bp DNA linear PAT 18-JUN-2001 Yeast capable of low-temperature regulation of activation and methods for preparation and utilization thereof.
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CI2N15/09,A21D8/04,A21D10/02,C12N1/19//C12N9/16,(C12N1/19, PC
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(Inclassified.)

Shun, H., Yoshinobu, K., Akio, O., Yukio, M., Tetsuji, T., Yoshie, Y.,

Kozo, O. and Yuto, T.

Yeast capable of low-temperature regulation of activation and
methods for preparation and utilization thereof

Patent: JP 1999042090, A 69 16-FEB-1999;

SHOWA SANGYO CO LTD, KANEKA CORP
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                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 66)

4 inley M., Armstrong, K., Belmar, S., Folkerts, O., Hopkins, N., Menke, M.A., Pareddy, D., Petolino, J.F., Smith, K. and Woosley, A. Regulatory sequences for transgenic plants

Patent: US 6384207-A 48 07-MAY-2002;
    Gaps
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                                               3030 ACAACCAGAACCAATAAACACCCCAACACACACAAAACAACAGT
                                                                                              1 ACAGGCAAAAAAAAAAAAAACCAAACAAAAAAAAAAAGT
12;
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Sequence 48 from patent US 6384207.
AR209041
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Search completed: December 3, 2002, 06:48:19 Job time: 15894 secs
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HOMO Sapiens ezrin gene, 3' acceptor end, partial intron 9.
AF053448
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 60)
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                                                                                                                                                           /organism="Hypomyces odoratus"
/isolate="685 111.92"
/specifc_host="Tricholoma terreum"
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                                                                                 Query Match 0.3%; Score 24.6; DB 6; Best Local Similarity 70.2%; Pred. No. 1.2e+06; Matches 33; Conservative 0; Mismatches 14;
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0.2%; Score 24.4; DB 8;
Best Local Similarity 63.8%; Pred. No. 1.3e+06;
Matches 37; Conservative 0; Mismatches 21;
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       /organism="unidentified"
/db_xref="taxon:32644"
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Majander-Nordenswan,P., Sainio,M., Turunen,O., Jaaskelainen,J.,
Carpen,O., Kere,J. and Vaheri,A.
Direct Submission
Submitted (01-DEC-1997) Haartman Institute, University of Helsinki, Haartmaninkatu 3 PL 21, Helsinki FIN-00014, Finland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            /map="6q25-q26; between 6D6S442 and D6S281"
/clone="Pl genomic clones #6096 and #6097 (Genome Systems,
Majander-Nordenswan,P., Sainio,M., Turunen,O., Jaaskelainen,J., Carpen,O., Kere,J. and Vaheri,A.
Genomic structure of the human ezrin gene Hum. Genet. 103 (6), 662-665 (1998)
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Best Local Similarity 78.4%; Pred. No. 1.4e+06;
Matches 29; Conservative 0; Mismatches 8;
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/note="ezrin; 3' acceptor"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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SNP oligonuc

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Human secreted pro Human secreted pro Mouse spliced tran Orangutan epsilon-Orangutan epsilon-Test sequence from

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pBR322 ori upstrea Oligo TG62 for cre

template

Human map-related

Oligonucleotide

Circular

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; eurorportective; antiinflacobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interferon; multifactorial disease; autoimmune disease; inflammation; nervous system disease; ss.
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AAC12223
AAC14733
ABN51781
AAQ69650
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ABN27757
AAQ06733
AAQ12932
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AAH40540
AAX15719
ABN51514
AAV76224
AAT65704
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24. (SIDS2/gcgdata/geneseq-embl/NAL999.DAT:*
25. (SIDS2/gcgdata/geneseq-embl/NAL999.DAT:*
26. (SIDS2/gcgdata/geneseq-geneseqn-embl/NAL999.DAT:*
27. (SIDS2/gcgdata/geneseq-embl/NAL999.DAT:*
28. (SIDS2/gcgdata/geneseq-embl/NAL999.DAT:*
29. (SIDS2/gcgdata/geneseq-embl/NAL999.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
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Compugen Ltd
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9766
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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(CURA-) CURAGEN CORP

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RESULT 3
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                                                   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
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Live 0; Mismatches
                                                                                                      Claim 1; Page 1565; 4143pp; English
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27-DEC-2000; 2000US-0173419.
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Shimkets RA, Leach
                         WPI; 2001-465210/50
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es 51; Conserv
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, anglopoietin, appoposis related proteins, cadherin, cytlin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, or protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune content of the protein such as autoimmune systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, content content of pathogenic contents), diseases of the nervous system and an infection of pathogenic
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Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g.
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Pred. No. 0.0068;
0: Mismatches 0; Indels
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                                                                        cancer, autoimmune diseases and infections -
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Matches 51; Conservative 0; Mismatches
                                                                                                                                                     Claim 1; Page 3083; 4143pp; English.
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27-DEC-2000;
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(CURA-) CURAGEN CORP.
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cancer, autoimmune diseases and infections
                                                                                  Claim 1; Page 3083; 4143pp; English.
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27-DEC-2000; 2000US-0173419.
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Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; Grprotein coupled receptor; thioesterase; intlammation; multifactorial disease; sutoimmune disease; infection;
The present invention relates to oligonucleotides encoding polymorphic availants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, coproteins, cytochromes, kinesins, cytokines, interferons, interleukins, one such oligonucleotides and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer of the hadder where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
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100.0%; Pred. No. 0.0068;
ive 0; Mismatches 0; Indels
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27-DEC-2000; 2000US-0173419.
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                                                                                              by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; eucroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoletin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
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apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytochines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded
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5. 0.0068;
0; Indels
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                                                                                                                                                                                                                                                                                                 Sequence 51 BP; 22 A; 7 C; 13 G; 9 T; 0 other;
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Pred. No. (
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G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumaticid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4-hydroxybutyrate; dehydrogenase; protein therapy; adenosine triphosphate-dependent RNA helicase; major histocompatibility complex Class I histocompatibility antigen; MHC; phosphoglycerate kinase; immunosuppressive; immunostimulatory; antitrenantic; antisclerotic; antidiabetic; antiliflammatory; cytostatic; antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 0.0068;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                          Sequence 51 BP; 20 A; 18 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 0.0 tive 0; Mismatches
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                         delutivity of proteins related to angiopoietin, 4 hydroxyburyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major histocompatibility complex (MHC) Class I histocompatibility antigen and/or phosphoglycerate kinase. Disorders that may be prevented, diagnosed and/or treated by the above methods include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erytheromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also
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     useful in gene/protein therapy, vaccines, modulation of the expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51 BP; 15 A; 16 C; 12 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strength, speed and endurance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; Conservative
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The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinasins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is

Claim 1; Page 1565; 4143pp; English.

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                by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus errythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopietin; apoptosis related protein; cabherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; cytokine; interferon; interfeuking Grototein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
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Pred. No. 0.017;
                                                                                                                                                                                                                         Sequence 51 BP; 23 A; 11 C; 9 G; 8 T; 0 other;
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27-DEC-2000; 2000US-0173419.
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Matches 50; Conservative
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above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
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Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                   Sequence 51 BP; 22 A; 11 C; 13 G; 5 T; 0 other;
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messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcriptome comprises messenger RNAs transcriptome comprises several oligonuclectides, each capable of hybridising selectively to a several oligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profilling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in checting RNA transcripts and splice variants of human or animal transcriptiones. The libraries may also be used as specialised minitaries to detect transcripts of a sub-transcriptome under a libraries to detect transcripts of a sub-transcriptome under a particular biological or pathology specific genes such as those genes conly expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a patiticular disorder. ARNZ7253 to ABNS9589 represent
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                 (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic
systemic lupus erythromatosus and Grave's disease), inflammation, cancer
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                                                                                                                                                                    Gaps
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splice variant; transcriptome; oligonucleotide library; ss.
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                                                                                                                               Length 51;
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                                                                                                                             Score 49.4; DB 22;
Pred. No 0.017;
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                                                                                                                                                                  Mismatches
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                                                                                                                                                                    Conservative
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                                                                                                                                                 Sest Local Similarity
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                                                                                           Sequence 51
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                                                          organisms
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2545 TACAAAATGACTTCTGGAGACAAAACTT 2575
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                   for this patent did not form part of the printed obtained in electronic format directly from WIPO
                                                                                                                                                                                          9358 AATGAAAAGACCCATGAAGACCTCCCCAGAGATGGACATTCAGAATCCAGATGATGGA 9417
                                                                                                                                                          Gaps
                                                                                                                                                                                                            New nucleic acid segment comprising one of the 10 - 100 bp sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid analysis; diagnosis; monitoring; heart disease; CNS disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid segments containing polymorphic sites, or complements and methods of detecting a nucleic acid - for general use including diagnosis and monitoring of diseases
                                                                                                                                                          ö
                                                                                                                    0.4%; Score 34.2; DB 24; Length 65; llarity 71.4%; Pred. No. 1.2e+02; Conservative 0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide fragment containing polymorphic site, WI-1011
                                                                                    BP; 24 A; 15 C; 18 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31 BP; 8 A; 4 C; 5 G; 13 T; 1 other;
     present invention.
                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipshutz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 17; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US04571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0042125.
97US-0813159.
the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                 AAV67602 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chee M, Fan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                N.B. The sequence data
specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; polymorphic site; cancer; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-495419/42.
                                                                                                                                      Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                             9418 GCC 9420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9838846-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-1997;
07-MAR-1997;
                                                                                      Sequence 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-1998
                                                                                                                                                                                                                                                                                             GCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                  AAV67602;
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berno A,
                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                 AAV67602,
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The present invention relates to Simple Sequence Repeats (SSRs) from clover species. SSRs, also called microsatellites, are based on a 1-7 mucleotide core element which is tandemly repeated. The SSR array is embedded in complex flanking DNB. SSRs are ideal markers for genome mapping, trait mapping and marker-assisted selection. The SSRs may be used in methods for selecting genes in clover/legume breeding. The SSRs are also useful for DNB profiling of clover varieties and for testing the purity of legume seed batches. The present sequence is a SSR motif, which was used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel simple sequence repeats in clover species useful for selection genes in legume breeding, for profilling legume species varieties and for testing the purity of legume seed batches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                     Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping; trait mapping; marker-assisted selection; gene selection; legume; DNA profiling; breeding; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6075 CACACACACACACAGAGAGAGACAGCAGGAGATGGAAAGAGCATCAAAGCG 6123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.3%; Score 28.2; DB 22;
73.5%; Pred. No. 3.7e+03;
Live 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58 BP; 28 A; 8 C; 22 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 35; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2001; 2001NZ-0509194
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2000; 2000AU-0006520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 73.50,
Thes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forster JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA64666 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-431058/46.
23-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          24-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koelliker R,
                                                    SSR motif #3
                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                  25-MAY-2001.
                                                                                                                                                                                                                                                              NZ509194-A.
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Gaps

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Indels

0.3%; Score 30.6; DB 19; 96.8%; Pred. No. 6.7e+02; tive 1; Mismatches 0;

Best Local Similarity 96.8 Matches 30; Conservative

Query Match

Length 31;

99US-0257417

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25-FEB-2000; 2000WO-US04929
                                          GOUT I.
RODNIN N.
FILONENKO V.
MATSUKA G.
SCANLAN M.
                      25-FEB-1999;
                                                                (FILO/)
(MATS/)
                                                                                      (SCAN/)
(OLDL/)
                                                                                                                                 Gout I,
                                            (COUT/)
                                                       RODN/)
                                                                                                                                                                                                                                                                                                                                                                                                                              36
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       Melanoma; thyroid tumour; MEL3; MEL7; Thy5; Thy6; Thy11; Thy14; Thy15; rectal cancer; lung cancer; breast cancer; colon cancer; PCR primer; Ki-67 nuclear antigen gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Melanoma; thyroid tumour; MEL3; MEL7; Thy5; Thy1; Thy11; Thy14; Thy15; rectal cancer; lung cancer; breast cancer; colon cancer; PCR primer; Ki-67 nuclear antigen gene; ss.
                                                                                                                                                                                                                                                                                                                                                          The specification describes polynucleotides which are associated with melanoma and thyroid tumors. Specifically, these are MEL3, MEL7, Thy5, Thy1. Thy14, and Thy15. The polynucleotides are useful for diagnosing and treating a patient with melanoma, thyroid tumour, rectal cancer, lung cancer, breast cancer or colon cancer. PCR primers AAA64666-67 were used to amplify a fragment of MEL-9 clone, which encodes a K1-67 nuclear antigen gene, which is a polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecules for diagnosing and treating melanoma, thyroid tumors, rectal, lung, breast and colon cancers
                                                                                                                                                                                                                                                     Old L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer used to amplify a 500 bp fragment of a MEL9 clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.3%; Score 27.8; DB 21; Length 53; 93.5%; Pred. No. 4.4e+03; ative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                     Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53 BP; 18 A; 21 C; 8 G; 6 T; 0 other;
                                                                                                                                                                                                                                                     Rodnin N, Filonenko V, Matsuka G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4316 AACAGAACTGGACCCAGCAGCAAGTGTAAC 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 ACCACAAACTGGACCCAGCAGCAAGTGTAAC 53
                                                                                                                                                                                                                                                                                                                                       Example 3; Page 48; 94pp; English
                                                                                                                      25-FEB-2000; 2000WO-US04929
                                                                                                                                           99US-0257417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .667/c
AAA64667 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                              GOUT I.
RODNIN N.
FILONENKO V.
                                                                                                                                                                                                                                                                                  WPI; 2000-572092/53
                                                                                                                                                                                              MATSUKA G.
SCANLAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                    OLD L.
BILYNSKY B.
                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention
                                                                         WO200050595-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200050595-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                      Homo sapiens
                                                                                                                                          25-FEB-1999;
                                                                                                31-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JAN-2001
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                                                                                                                                                                                    (FILO/) E (MATS/) N (SCAN/) S (OLDL/) C (BILY/) E
                                                                                                                                                                                                                                                               Bilynsky
                                                                                                                                                                GOUT/)
                                                                                                                                                                           RODN/)
                                                                                                                                                                                                                                                     Gout I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
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melanoma and thyroid tumors. Specifically, these are MEIJ, MEIJ, Thys, Thys, Thyll, Thyll, and Thyls. The polynucleotides are useful for diagnosing and treating a patient with melanoma, thyroid tumour, rectal cancer, lung cancer, breast cancer or colon cancer. PCR primers AAA64666-67 were used to amplify a fragment of MEL-9 clone, which encodes a Ki-67 nuclear antigen gene, which is a polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                  The specification describes polynucleotides which are associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                             Novel isolated nucleic acid molecules for diagnosing and treating melanoma, thyroid tumors, rectal, lung, breast and colon cancers
                                                                            01d L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 36;
                                                                            Scanlan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.4; DB 21;
Pred. No. 4.6e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 BP; 7 A; 10 C; 8 G; 11 T; 0 other;
                                                                         Rodnin N, Filonenko V, Matsuka G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: December 3, 2002, 02:19:34 Job time : 1189 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7279 CCTAAGGAAAAGGCTGAGGCTCTAGAGGA 7307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 96.6
Matches 28; Conservative
                                                                                                                                                           WPI; 2000-572092/53
                      (BILY/) BILYNSKY B
OLD L
                                                                                                     Bilynsky B;
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Appl Appl Appl Appl Appl Appli Appli Appli

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence

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ALIGNMENTS

Sequence Sequence Sequence

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GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Tarin, Lisa M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Molecules, Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
US-08-689-856-22
US-09-415-784-32
US-08-9415-785A-32
US-08-125-900-32
US-09-415-868-32
US-09-415-868-32
US-09-415-868-32
US-09-19-25
US-08-273-594-34
US-08-273-594-34
US-09-094-919-34
US-09-91-24-13
US-09-091-814-74
US-08-459-610-24
US-08-459-610-24
US-08-459-610-24
US-08-459-610-24
US-08-373-594-24
US-08-373-594-24
US-08-373-594-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genelabs Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-UNN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/081,070 FILING DATE: 22-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/171,389 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 400, Application US/08171389
Patent No. 5578444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 40C
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fabian, Gary R. REGISTRATION NUMBER:
     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Genelabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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 RESULT 1
                        0 0 0 0 0 0 0 0 0 0 0
                                                                                                                     2, 2002, 22:44:20 ; Search time 191 Seconds (without alignments) 15680.656 Million cell updates/sec
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being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, 7
Sequence 48, 8
Sequence 13, 8
Sequence 10, 8
Sequence 10, 8
Sequence 10, 8
Sequence 10, 8
Sequence 20, 8
Sequence 20, 8
Sequence 29, 8
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Sequence 400,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/AB_COMB.seq:*
/cgn2_6/ptodata/1/ina/BD_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-475-228A-400
US-08-475-228A-400
US-08-475-228A-400
US-09-354-947-400
PCT-US93-12388-400
US-08-207-901-33
US-08-207-901-13
US-08-123-177A-56
US-08-133-11-13
US-08-438-511-13
US-08-438-511-16
US-08-438-511-16
US-08-438-511-16
US-08-438-511-16
US-08-438-511-16
US-08-438-511-16
US-08-438-511-178-29
US-08-805-631A-29
US-08-805-631A-29
US-08-222-177A-169
US-08-222-177A-169
US-08-222-177A-169
US-08-221-177A-169
US-08-481-710-67
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US-08-222-177A-256
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -0896-09537-67
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                                                                                                                                                                                                                                                                                                                          441362 segs, 153338381 residues
                                                                                                                                                                                         US-09-700-906A-1_COPY_197_9962
9766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                         - nucleic search, using sw model
                                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*
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                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 66
                                                                                                                           December
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                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                           Run on:
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Gaps

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10; Indels

Length 50;

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Orangutan epsilon-globin gene with flanking Alu repeats
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APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPLICATION NUMBER: 05-000-1995
FILING DATE: 06-000-1995
PROOR APPLICATION NUMBER: 06-000-1995
PROOR APPLICATION DATA:
APPLICATION NUMBER: 17-SEP-1993
PROOR APPLICATION DATA:
APPLICATION NUMBER: 03-006,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: 03-007/23,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: 27-JUN-1991
PRIOR APPLICATION NUMBER: 05-007/23,618
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Strattford, carol A.
REGISTRATION NUMBER: 34,444
REGISTRATION NUMBER: 34,444
                                                                                                        6062 CGTCAGGGAAGACCACACACACACAGAGACACAGGA 6102
                                                                                                                                                    9 CGGCAGTGAAGAATAAAAGGCCACACAGAGAGGCAGCAGCA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                  DB 1; L
1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.3%; Score 25; DB 2; 75.6%; Pred. No. 1.1e+03;
                                                             Mismatches
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               Score 25;
Pred. No. 1
                                                                                                                                                                                                                                                           Sequence 400, Application US/08475228A patent No. 5869241 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 400
                  Query Match 0.3%;
Best Local Similarity 75.6%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSE: Genelabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: EGWARGS, Cynthia A.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of TITLE OF INVENTION: Days Building Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
                                                                                                                                                  ; INDIVIDUAL ISOLATE: Orangutan epsilon-globin gene with INDIVIDUAL ISOLATE: flanking Alu repeats US-08-171-389-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orangutan epsilon-globin gene with flanking Alu repeats
                                                                                                                                                                                                                                      Query Match 0.3%; Score 25; DB 1; Length 50; Best Local Similarity 75.6%; Pred. No. 1.1e+03; Matches 31; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                               6062 CGTCAGGGAAGACCACACACACACAGAGAGAGACAGCAGGA 6102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
                                                                                                                                                                                                                                                                                                                                                        9 CGGCAGTGAAGAATAAAAGGCCACACAGAGAGAGAGCAGCAGCAGCA 49
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REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 400:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genelabs Technologies, Inc.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 Penobscot Drive
                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
50 base pairs
                                             double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE: ; INDIVIDUAL ISOLATE: US-08-123-936-400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 500 contract Redwood City
                         nucleic acid
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                      TYPE: nucleic
STRANDEDNESS:
                                                                                                                                  ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94063
                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-123-936-400
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LENGTH:
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Pred. No. 1.1e+03;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Edwards, Cynthia A.

APPLICANT: Cantor, Charles R.

APPLICANT: Tarin, Lisa M.

APPLICANT: Fry, Kirk E.

TILLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
6062 CGTCAGGGAAGACCACACACACACACAGAGAGACAGCAGGA 6102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4600-0175.20/G19P3D1
                                     9 CGGCAGTGAAGAATAAAAGGCCACACAGAGAGGGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genelabs Technologies, Inc
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APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY APPLICATION NUMBER: US 08/081,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          Sequence 400, Application US/09354947 Patent No. 6384208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technolc
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39,118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.3
Best Local Similarity 75.6
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brady, John F. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                          RESULT 5
US-09-354-947-400
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                                                            Q
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Andrews, Beth M.
APPLICANT: Trin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.3%; Score 25; DB 3; Length 50; 75.6%; Pred. No. 1.1e+03; Live 0; Mismatches 10; Indels
                          6062 CGTCAGGGAAGACCACACAGACACAGAGAGAGAGAGGA 6102
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4600-0175.20/G19P3D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/482,080A FILING DATE: 07-JUN 1995 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/171,389 FILING DATE: 20-DEC-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/123,936 FILING DATE: 17-SEP-1993 PRIOR APPLICATION NUMBER: US 07/996,783 FILING DATE: 23-DEC-1992 PRIOR APPLICATION NUMBER: US 07/723,618 FILING DATE: 27-JUN-1991 PRIOR APPLICATION NUMBER: US 08/081,070 FILING DATE: 22-JUN-1991 ATPOLEMENTOR NUMBER: US 08/081,070 FILING DATE: 100-2014 ATPOLEMENTOR NUMBER: US 08/081,070 FILING DATE: 100-2
                                                                                                                                                                                                                                                  Sequence 400, Application US/08482080A Patent No. 6010849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0860
INFORMATION FOR SEQ ID NO: 400
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.3
Best Local Similarity 75.6
Matches 31; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
COUNTRY: US
ZIP: 94063
                                                                                                                                                                                                                    US-08-482-080A-400
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Gaps

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FITLE OF INVENTION: AMPLIFICATION IN NUCLEIC ACID HYBRIDIZATION ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2073 ACCTGCTACTCCAAAGAAGCCTGTGGGCGAAGTTCACAGTCAATTT 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 ACCACTTTCTCCAAAGAAGCCTATGGGAGKGGGCCTCAGYCCGTTT 4
                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.8; DB 1;
Pred. No. 1.2e+03;
1; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DowElanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/639,560B
FILING DATE: 10-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Armitoy, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkeris, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A
APPLICANT: Pareddy, Dayakar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-097-319A-48
; Sequence 48, Application US/09097319A
: Patent No. 6384207
                   NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34,174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: 510-655-3542
                                                                               4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-207-901-43
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Best Local Similarity 69.6%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Kenneth M. REGISTRATION NUMBER: 34,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RENUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                        CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6384207
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Indiana
COUNTRY: USA
                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                   ZIP: 94608
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TELEX: N/
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APPLICANT:
APPLICANT:
                                                                                                                                               COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Urdea, Michael S.
ATILE OF INVENTION: USE OF DNA-DEPENDENT RNA FOLYMERASE
TITLE OF INVENTION: TRANSCRIPTS AS REPORTER MOLECULES FOR SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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75.6%; Pred. No. 1.1e+03;
tive 0; Mismatches 10; Indels
                                                                                                                                                                                                                               TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and Methods NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
                 6062 CGTCAGGGAAGACCACACACACACAGAGAGACAGCAGGA 6102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6062 CGTCAGGGAAGACCACACAGACACAGAGAGAGACAGCAGGA 6102
                                            9 CGGCAGTGAAGAATAAAAGGCCACACAGAGAGGCAGCAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/12388
                                                                                                                                                               Sequence 400, Application PC/TUS9312388 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 400:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/08207901
Patent No. 5629153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity 75.69
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                           PCT-US93-12388-400
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US-08-207-901-43/c
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Gaps
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Smith, Kelley
Woosley, Aaron
YENTION: Regulatory Sequences for Transgenic Plants
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Length 50;
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IMMEDIATE SOURCE:
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                        ; CLONE: mfc
US-08-222-177A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
ADDRESSE: DeWitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.3%; Score 24.8; DB 4; Length 66; Best Local Similarity 63.3%; Pred. No. 1.5e+03; Matches 38; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                  SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30,492
ER: 09865.601
                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-222-177A-56

US-08-222-177A-56

Sequence 56, Application US/08222177A

Patent No. 5582979

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               APPLICATE APPLIANCE DATE:
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                              LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA
US-09-097-319A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Madison
STATE: Wisconsin
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                            linear
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                                       SOFTWARE:
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APPLICANT: Chivers, Mark L.
APPLICANT: Belval, Thomas K.
TITLE OF INVENTION: Method for the Rapid Removal of
TITLE OF INVENTION: Protoporphyrin IX from Protoporphyrin IX-Containing Solutio
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                   Gaps
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  Length 62;
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                                                 Indels
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                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
                                                 13;
0.2%; Score 24.2; DB 1;
71.1%; Pred. No. 2.1e+03;
tive 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: primer for pBR322 ori positions MOLECULE TYPE: 3170-3148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,071
FILING DATE: NO. 5665869ember 15, 1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                   APPLICANT: Ryland, James R.
APPLICANT: Matthews, Maura-Ann H.
APPLICANT: Ernst, Ulrich P.
APPLICANT: Houk, Daniel E.
APPLICANT: Traylor, David W.
APPLICANT: Williams, Lee R.
APPLICANT: Mitchell, David J.
                                                                                                                                                                                                                                                  Sequence 13, Application US/08153071 Patent No. 5665869 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: NO. 5665869ember CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 56658698k, Henry P. REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Somatogen, Inc.
5797 Central Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
  Query Match 0.29
Best Local Similarity 71.19
Matches 32; Conservative
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TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boulder
STATE: Colorado
ZIP: 80301
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MOLECULE TYPE: primer for pBR322 or1 positions 3170-3148 HYPOTHETICAL: no
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Pred. No. 2.2e+03;
0; Mismatches 15; Indels
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APPLICANT: Mathews, Antony J.
APPLICANT: Trimble, Stephen P.
APPLICANT: Anthony-Cahill, Spencer
TITLE OF INVENTION: Modified Hemoglobin-like Compounds
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage computer: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,511
FILING DATE: 10 May 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339,304
FILING DATE: 10, 5840851ember 14, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/097,273
FILING DATE: July 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5840851elli, Marianne F.
REGISTRATION NUMBER: 38571
REGISTRATION NUMBER: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette, 3.50 inch, 1.4 Mb storage
2545 Central Avenue, Suite FD1
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OPERATING SYSTEM: System 7.5
SOFTWARE: Microsoft word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3324
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Best Local Similarity 68.8
Matches 33; Conservative
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ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: Apple Macint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 303-444-3013 INFORMATION FOR SEQ ID NO:
                                                           Colorado
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                               Boulder
                                                                                       80301
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   Sequence 20, Application US/08609271
Patent No. 5811264
GENERAL INFORMATION:
APPLICANT: Altken, Jacqueline F.
APPLICANT: Lippincott, Julie A.
APPLICANT: Lopincott, Julie A.
APPLICANT: Lo
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no
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Pred. No. 2.2e+03;
0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Neway, Justin O.
TITLE OF INVENTION: Purification of Hemoglobin NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Somatogen, Inc.
STREET: 2545 Central Avenue, Site FD-1
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/188,374
FILING DATE: 1/27/94
ATTORNEY/AGENT INFORMATION:
NAME: No. 5811264elli, Marianne F.
REGISTRATION NUMBER: 38571
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 170/Div
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3324
TELEFAX: 303-444-3013
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Ryland, James R.
Matthews, Maura-Ann H.
Traylor, David W.
Milne, Erin E.
Durfee, Steven L.
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Patent No. 5840851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mathews, Antony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.2%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 68.88
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                CITY: BOULUCE
STATE: Colorado
ZIP: 80301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
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APPLICANT:
US-08-609-271-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-609-271-20
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APPLICANT:
APPLICANT:
APPLICANT:
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Trimble, Stephen

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Sequence 20, Application US/08188374B

Patent No. 6140071

GENERAL INFORMATION:

APPLICANT: Aitken F. Jacqueline

APPLICANT: Apostol, izydor Z.

APPLICANT: Lippincott, Julie A.

APPLICANT: Levine, Joseph D.

TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth

FILE REFERENCE: BXTB 1953

CURRENT APPLICATION NUMBER: US/08/188,3374B

CURRENT FILING DATE: 1994-01-27

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20

LENGTH: 54
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, OTHER INFORMATION: Description of Artificial Sequence: primer for ori;
, OTHER INFORMATION: pBR322 positions 3170-3148
US-08-188-374-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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0
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MOLECULE TYPE: primer for pBR322 ori positions 3170-3148
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.2%; Score 24; DB 2; Length 54; 68.8%; Pred. No. 2.2e+03; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.2%; Score 24; DB 3; Length 54; Best Local Similarity 68.8%; Pred. No. 2.2e+03; Matches 33; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AAAAGGATCCAAGTAGCCGGCGCCGCGTTCCACTGAGCGTCAGACCC 53
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                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,712
APPLICATION NUMBER: 08/240,712
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Theresa A.
REGISTRATION NUMBER: 32,547
REFERENCE/DOCKET NUMBER: 61
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-973-629-16
; Sequence 16, Application US/08973629A,
patent No. 6150506
; GENERAL INFORMATION:
                                                                                                                                                                                                                                   NAME: Ramsey R. Stewart
REGISTRATION NUMBER: 38,322
REFRENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541.3356
TELEFAX: 303-444-3013
June 7, 1995
N: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.29
Best Local Similarity 68.89
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 54
TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-188-374-20
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APPLICANT: Mathews, Anthony

APPLICANT: Mathews, Anthony

APPLICANT: Kerwin, Bruce

APPLICANT: Anthony-Cahill, Spencer

APPLICANT: Anthony-Cahill, Spencer

APPLICANT: Anthony-Cahill, Spencer

APPLICANT: Madril, Dominic

APPLICANT: Madril, Description of Artificial Sequence:

CURRENT FILING DAME: 1998-08-24

CURRENT FILING DAME: 1998-08-24

CURRENT FILING DAME: 1998-08-24

SEQ ID NO 16

SEQ ID NO 16

SEQ ID NO 16

CORGANISM: Artificial Sequence

CORGANISM: Artificial Sequence

COTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Digonucleotide or 5' primer for production of a

OTHER INFORMATION: Description of Mismatches 15; Indels

OURTY Match

Best Local Similarity 68-8%; Pred. No. 2.2e+03;

Matches 33; Conservative 0; Mismatches 15; Indels

OURTY MATCH

Best Local Similarity 68-8%; Pred. No. 2.2e+03;

Matches 33; Conservative 0; Mismatches 15; Indels

ON 31 AAAAGGATCCAAGGGCCCCCCCTGAGCCCCACTACCCAGACCC 53

ON AAAAGGATCCAAGAGCGCGCGCCCCCACTACCCTGAGCCCACTACCAGACCC 53

AND AAAAGGATCCAAGAGCCGCGCCCCCACTACCACTGAGCCCCACTACCACTGAGCCCC 53
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Search completed: December 3, 2002, 02:23:04 Job time: 199 secs

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December 3, 2002, 02:01:16 ; Search time 244 Seconds (without alignments) 15414.088 Million cell updates/sec
                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                             341543 seqs, 192557720 residues
                                                                                                                                                                                                                            US-09-700-906A-1_COPY_197_9962
9766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 66
                                                                                                                                                                                                                                        Title:
Perfect score:
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Maximum DB :
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpna/US09_NBW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US09_LUBCOMB.seq:*/cgn2_6/ptodata/1/pubpna/US10_NBW_PUB.seq:*/cgn2_6/ptodata/1/pubpna/US10_LUBCOMB.seq:*

SUMMARIES

Result No.	Score	Query Match 1	Duery Match Length DB	DB	ID	Description
c 1	25.4	0.3	64	10	US-09-983-965-4203	Sequence 4203, Ap
7	23.4	0.5	61	6	US-09-946-807-1349	Sequence 1349, Ap
33	23.4	0.3	61	10	US-09-795-668-1349	Sequence 1349, Ap
4	23.4	0.5	61	10	US-09-795-686-1349	Sequence 1349, Ap
n n	23.2	0.3	49	10	US-09-896-915-31	Sequence 31, Appl
9	23.2	0.5	64	10	US-09-919-580-637	Sequence 637, App
7	22.6	0.5	62	10	US-09-919-580-175	Sequence 175, App
8	22.6	0.5	62	10	US-09-983-965-4296	Sequence 4296, Ap
σ	22.4	0.5	64	10	US-09-983-965-42	Sequence 42, Appl
3 10	22.2	0.3	47	10	US-09-263-959-514	Sequence 514, App
c 11	22.2	0.3	63	10	US-09-983-965-5096	Sequence 5096, Ap
12	22	0.2	9	σ	US-10-057-940-14	Sequence 14, Appl
13	21.8	0.3	47	σ	US-09-978-295A-378	Sequence 378, App
14	21.8	0.5	4.7	σ	US-09-978-697-378	Sequence 378, App
15	21.8	0.5	54	10	US-09-982-610-42	Sequence 42, Appl
16	21.8	0.5	99	10	US-09-983-965-64	Sequence 64, Appl
17	21.4	0.5	53	10	US-09-783-590-3220	Sequence 3220, Ap
3 18	21.4	0.2	63	10	US-09-878-574-2344	
19	21.2	0.5	47	10	US-09-765-527-244	

Sequence 19, Appl Sequence 50, Appl Sequence 89, Appl Sequence 741, App Sequence 195, App Sequence 195, App Sequence 195, App Sequence 135, App Sequence 1332, App Sequence 1332, App Sequence 16, Appl Sequence 6, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 170, Appl Sequence 70, Appl Sequence 70, Appl Sequence 70, Appl Sequence 188, Appl Sequence 188, Appl Sequence 194, Appl Sequence 194, Appl Sequence 194, Appl Sequence 194, Appl Sequence 1294, Appl Sequence 1	
US-09-836-077-19 US-09-320-337-50 US-09-925-012-98 US-09-919-580-741 US-09-919-580-741 US-09-918-965-299 US-09-918-965-299 US-09-918-965-399 US-09-918-965-395 US-09-944-035-305 US-09-946-807-1332 US-09-946-807-1332 US-09-946-807-1332 US-09-946-807-1332 US-09-946-807-1332 US-09-946-807-1332 US-09-999-255-311-788 US-09-989-205-311-758 US-09-983-965-97	
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US-09-993-955-42013

US-09-993
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SOFTWARE: FastSEQ for Windows Version 4.0
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                    SEQ ID NO 1349
LENGTH: 61
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                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 61;
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.2%; Score 23.4; DB 9; Best Local Similarity 61.0%; Pred. No. 1.2e+04; Matches 36; Conservative 1; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1349, Application US/09795668
Patent No. US20020045577A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Gulcher, Jaffrey R.
ITLE OF INVENTION: HUMAN SCHIZOPHENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
FILE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFRENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
                    APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
                                                                            CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR PILING DATE: 2001-02-28
PRIOR PLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1349
Steinthorsdottir, Valgerdur
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                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-946-807-1349
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ORGANISM: Homo sapiens
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US-09-795-668-1349
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US-09-795-686-1349
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Pyle, Ruth
APPLICANT: Yu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
CURRENT APPLICATION NUMBER: US/09/919,580
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                     Length 61;
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                                                                                                                  Indels
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                                                                     DB 10;
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Pred. No. 1.2e+04;
0; Mismatches 13;
                                                                  Score 23.4; DB 1
Pred. No. 1.2e+04
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Medical Research Council
APPLICANT: Griffiths, Andrew
TITLE OF INVENTION: Optical Sorting Method
FILE REFRENCE: 18396/2022
CURRENT APPLICATION NUMBER: US/09/896,915
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1999-01-06
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Oligonucleotide FLAGas US-09-896-915-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 637, Application US/09919580 ; Patent No. US20020110832A1
                                                                                                                                                                                                                                                                                                                           Sequence 31, Application US/09896915 Patent No. US20020119459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 56
OTHER INFORMATION: n = A,T,C or G
                                                                     0.2%;
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Best Local Similarity 70.5%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                Query Match 0.2%
Best Local Similarity 61.0%
Matches 36; Conservative
; ORGANISM: Homo sapiens US-09-795-686-1349
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34; Conservative
       Best Local Similarity
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ZIP: 98104-7092
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US-09-263-959-514/c
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APPLICANT: Tao., Nengbing
APPLICANT: Tao., Nengbing
APPLICANT: Mathabagan, Nagapan
TITLE DE INVENTION: UNCLEIC AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT PILING DATE: 2001-10-26
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
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                                                                                                                                                                                                             9317 CTGAGGTCTTTGTATTAGCAGAAAGAATAGAAATAAACAGAAATGAAAAGAAG 9369
                                                                                                                                                                                                                                                                                                                                                                              US-09-919-580-175/C

US-09-919-580-175/C

Sequence 175, Application US/09919580

Sequence 175, Application US/09919580

Sequence 175, Application US/09919580

Setent No. US-00200110832al

Setent No. US-00200110832al

APPLICANT: Pyle, Ruth

APPLICANT: Yu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REPERBNCE: 21012.1.552

CURRENT APPLICATION NUMBER: US/09/919,580

CURRENT APPLICATION NUMBER: US/09/919,580

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FRASEQ for Windows Version 4.0

FENCENTIAL OF TEXTS OF TE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9321 GGTCTTTGTATTAGCAGAAGAATAGAAATAAACAGAAATGAAAAGAA 9368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 63-LIB3058-027-Q1-K1-H4
US-09-983-965-4296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22.6; DB 10;
Pred. No. 2e+04;
0; Mismatches 17;
                                                                     DB 10;
                                                              Query Match 0.2%; Score 23.2; DB 10 Best Local Similarity 64.2%; Pred. No. 1.4e+04; Matches 34; Conservative 0; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22.6;
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; Patent No. US20020137160A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: 46, 47, 52
; OTHER INFORMATION: n = A,T,C or G
US-09-919-880-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.2%;
ilarity 64.6%;
Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 31; Conserv
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US-09-919-580-637
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LENGTH: 62
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byat, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
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Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
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                           Gaps
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                                                                2789 AGACATATAAGGAAAATATTGAATTAAAAGAAAACGATGAAAAGATGAAAGCA 2841
                                                                                       Length 64;
                      19; Indels
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; OTHER INFORMATION: Clone ID: 05-BOVMS1-021-Q1-E1-B1
US-09-983-965-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22.4; DB 10;
Pred. No. 2.3e+04;
0; Mismatches 26;
64.2%; Pred. No. 2e+04; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OVETWARE: PATEBLIAN SOFTWARE: PATENTAIN APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     ; Sequence 42, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.2%;
Best Local Similarity 59.4%;
Matches 38; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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ORGANISM: Bos taurus
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2002-05-03
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  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-978-295A-378
                                                                                                                                                                                                                                                                                 US-10-057-940-14
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Patent No. US20020137160A1
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
GENERAL INPORMATION:
Harten, Wesley C.
APPLICANT: Pact, Vohn C.
APPLICANT: Patt, John C.
APPLICANT: MATHIBLE OF INVENTION: WUCKEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983, 965
CURRENT FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NOS: 5912
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APPLICANT: Pantoliano, Michael W.
APPLICANT: Salemme, F. Raymond APPLICANT: Carver, Jr., Theodore, E.
TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
TITLE OF INVENTION: Identified Using a Genomics Approach
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                                                                                                                                                                                                                                                                                                                                                Length 47;
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US-09-983-965-5096
                                                                                                                                                                                                                                                                                                                                         Query Match 0.2%; Score 22.2; DB 10; Best Local Similarity 69.8%; Pred. No. 2.1e+04; Matches 30; Conservative 0; Mismatches 13;
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61.0%; Pred. No. 2.5e+04;
tive 0; Mismatches 23;
                                                          REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 920010.426C2
REERERENCAPOOKERT NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO. 514:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CURRENT APPLICATION NUMBER: US/10/057,940
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                 ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.0°
Matches 36; Conservative
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CLASSIFICATION:
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US-10-057-940-14/c
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US-09-263-959-514
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OTHER INFORMATION: T- and A-rich tract with single-stranded and duplex DNA
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                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                     Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.2%; Score 22; DB 9; 167.4%; Pred. No. 2.7e+04;
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PRIOR APPLICATION NUMBER: 09/190,128
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION UNMBER: US 60/065,129
PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR PRILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
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Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
                                                                                                 NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 60
                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Filvaroff, Ellen
Fong, Sherman
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Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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NUMBER: 60/077632 1998-03-11 1998-03-11 1998-03-11 1998-03-11 NUMBER: 60/077649 1998-03-12 1998-03-12 1998-03-12 NUMBER: 60/07791 1998-03-20 NUMBER: 60/07886 1998-03-20 NUMBER: 60/07886 1998-03-20 NUMBER: 60/07896	NAMBER 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7 1998-7	1998 - 0.4 -
APPLICATION FILING DATE: APPLICATION APPLICATION FILING DATE: APPLICATION FILING DATE: FILING DATE: APPLICATION APPLI	ATTION AT	FILLING DATE: APPLICATION
PRIOR	PRIOR	PRIOR

PRIOR FILING DATE: 1998-04-12
PRIOR FILING DATE: 1998-04-22
PRIOR PRILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08204
PRIOR PLING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR APPLICATION NUMBER: 60/082796
PRIOR APPLICATION NUMBER: 60/082796
PRIOR APPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/08332
PRIOR PRILING DATE: 1998-04-23
PRIOR PRILING DATE: 1998-04-23
PRIOR PRILING DATE: 1998-04-29
PRIOR PRILING DATE: 1998-05-06
PRIOR PRILING DATE: 1998-05-06
PRIOR PRILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998 03-19
PRIOR APPLICATION NUMBER: 60/07886
PRIOR PAPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR PALICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELLNG DATE: 1998-03-20
PRIOR PELLNG DATE: 1998-03-20
PRIOR PELLNG DATE: 1998-03-20
PRIOR PELLNG DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079664
PRIOR PELLNG DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079669
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PRIOR APPLICATION NUMBER: 60/079669
PRIOR PELLNG DATE: 1998-03-27
PRIOR PELLNG DATE: 1998-03-37
PRIOR APPLICATION NUMBER: 60/079786
PRIOR PELLNG DATE: 1998-03-37
PRIOR PELLNG DATE: 1998-03-37
PRIOR APPLICATION NUMBER: 60/079786
PRIOR APPLICATION NUMBER: 60/079928
PRIOR PELLNG DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079928
PRIOR PELLNG DATE: 1998-03-30
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PRIOR PELLING DATE: 1998-03-31
PRIOR PELLING DATE: 1998-03-31
PRIOR PELLING DATE: 1998-03-31
PRIOR PELLING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR PELLING DATE: 1998-03-31
PRIOR PELLING DATE: 1998-03-31
PRIOR PELLING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080329
PRIOR PELLING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR PELLING DATE: 1998-04-01
PRIOR PELLING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR PELLING DATE: 1998-04-01
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PRIOR PELLING DATE: 1998-04-01
                            APPLICATION NUMBER: 60/078004
FILLIG DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
FILLING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/082569
FILING DATE: 1998-04-21
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PRIOR APPLICATION UNDBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
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PRIOR APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/081952
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PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/082568
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FILING DATE: 1998-04-22
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CURRENT APPLICATION NUMBER: US/09/9855

PRIOR FILING DATE: 2001-10-16

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-11-07

PRIOR FILING DATE: 1997-11-07

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-13

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PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 1997-11-14

PRIOR FILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-11

PRIOR FILING DATE: 1998-03-11
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                                                                                                                                                                                                                                                                                                                                    3610 TTACCTGGCAGCAAAGACAGCTACAGACTCCT 3642
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Goddard, Audrey
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Patent No. US20020169284A1
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FILING DATE: 1998-03-11
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FILING DATE: 1998-03-11
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Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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Filvaroff, Ellen
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Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
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Kuo, Sophia S.
Napier, Mary A.
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US-09-978-697-378
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PRIOR APPLICATION NUMBER: 60/08204
PRIOR FILING DATE: 1998-04-20
PRIOR FILING DATE: 1998-04-20
PRIOR FILING DATE: 1998-04-20
PRIOR PELING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/08339
PRIOR PELING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08356
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-39
PRIOR PELING DATE: 1998-04-39
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08539
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08539
PRIOR PELING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08539
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-13
PRIOR PELING DATE: 1998-05-15
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APPLICATION NUMBER: 60/085697

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Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
MOMBER OF SEQUENCES: 45
                                       0;
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Pred. No. 2.9e+04;
0; Mismatches 17; Indels
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  Length 47;
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                                       Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Score 21.8; DB 9;
Pred. No. 2.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/22616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INPORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0821P3PCT
                                                                          3610 TTACCTGGCAGCAAAAGACAGCTACAGACTCCT 3642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/">doi.org/10.1007/</a>
                                       0; Mismatches
                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 3, 2002, 09:05:14 Job time: 260 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,648
FILING DATE: 1996-MAY-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  Sequence 42, Application US/09982610 Patent No. US20020146420A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                                                Bennett, Brian D.
Goeddel, David
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                                                                                                                                                                                                                                                                                APPLICANT: Genentech, Inc
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0.2%;
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INFORMATION FOR SEQ ID NO: 42
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STRANDEDNESS: Sing
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Best Local Similarity 65.39
Matches 32; Conservative
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                                       Conservative
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                  Best Local Similarity
Matches 26; Conserv
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US-09-982-610-42
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Scoring table:

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.

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AL632972 AL632972
AL788410 ZM0035P22
AL734487 TETRACHOOD
AZ953243 ZM0218G21
AL464694 T. Brucei
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AZ314357 IM0031E10

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AZ314350 IM0031E20

AZ314350 IM0031E223

AZ659694 IM00337F13
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IMAGE:113755 3' similar to SP:B48666 B48666 CELL PROLIFERATION
ANTIGEN KI-67, SHORT FORM - ;, mRNA sequence.
                                                   AI887645 wm16d11.x
AZ375608 1M0129M04
BF663117 602145034
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                                                AIBR7645
AZ375608
BE653117
AA215584
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AA242896
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AZ815499
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CNS03JF6
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DEFINITION
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ORGANISM
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T76979/c
LOCUS
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KEYWORDS
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AZ456727 1M0259D17
AU267450 AU267450
AJ443729 AJ443729
AZ777647 2M0012N23
                                                                     2, 2002, 23:47:05 ; Search time 7932 Seconds (without alignments) 19940.132 Million cell updates/sec
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                                                                                                                                      1 atgtggcccacgagacgcct......tcatagggacagtgaagata 9766
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                                                                                                                                                                                                                 176248
        5.1.3
Compugen Ltd.
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           16154066 seqs, 8097743376 residues
                                                                                                             US-09-700-906A-1_COPY_197_9962
9766
          GenCore version
Copyright (c) 1993 - 2002
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                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                                                           summaries
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AA876462
AZ456727
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Maximum Match 100
Listing first 45
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gb_est4:*
gb_est5:*
em_estfun:*
em_estom:*
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em_gss_pln:*
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em_gss_rod:*
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Match I
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EST 15-MAR-1995

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Result

36.8 28.4 26.8 25.8 25.8

024331

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AA053228 zf53a06.s AZ589795 1M0399G01 W52237 zc50a07.s1

/clone="IMAGE:1252869"

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Query Match
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AZ456727/C
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ORIGIN
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                                                                                                                                                                                                                                                                                               11 bp mRNA linear EST 25-MAR-1998 similar to SW: CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1252869 similar to SW:KI67_HUMAN P46013 ANTIGEN KI-67.;, mRNA sequence. AA876462 GI:2985539 EST.
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GSP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                            /clone="IMAGE:113755"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.4%; Score 36.8; DB 14; Length 52; 82.0%; Pred. No. 4.2e+03; Live 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9485 ATGAGAGCTCCCAGCCTAAGGTGGCAGAGGAGAGGGGGAGGGCAGAAGAGT 9534
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                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:469372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo saplens"
/db_xref="taxon:9606"
                                                                                                                         High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                    Seg primer: -21m13
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Matches 41; Conservative
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KEYWORDS
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/note="Vector: PWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A2456727 47 bp DNA linear GSS 04-0CT-2000 1M0259D17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0259D17 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                         /note="Vector: pawPl0; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 4)

Unun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                       ö
                                           /tissue_type="metastatic prostate bone lesion"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                   Length 31;
                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                Score 28.4; DB 9;
Pred. No. 1.7e+05;
0; Mismatches 1;
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/clone_lib="NCI_CGAP_Pr12"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 10000 Std Error: (Plate: 0259 row: D column: 17 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism "Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC1M0259D17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ456727
AZ456727.1 GI:10614852
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Best Local Simira
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2M0012N23F Mouse 10kb plasmid UGG1M library Mus musculus genomic
clone UUGG2M0012N23 F, DNA sequence.
AZ777647
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University of Utah Genome Center
University of Utah
WR. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 62)
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                                                                               Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 57)
Buerstedde,J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                          Gallus gallus bursal lymphocyte EST
Contact: Buerstedde JM
Collular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 2025! Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2764 ATGAAGGAAATAGAAAGACCTTTTGAGACATATAAGGAAAATATTGAATTAAA 2816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 0.3%; Score 25.8; DB 9; Length 57; 1 Similarity 67.9%; Pred. No. 6.4e+05; 36; Conservative 0; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="CB"
/db_xref="taxon:9031"
/clone="37g1111"
/clone_lib="dkfa426"
/tissue_type="Bursa of Fabricius"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
a 10 t
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Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
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Location/Qualifiers
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Unpublished (2000)
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Fax: 801 585 7177
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                                                    chicken.
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adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (qi|q732114|qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells chemically-competent E. 21 to 22 to 23 to 23 to 24 to 25 to 
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1 (bases 1 to 55)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 0.3%; Score 26.8; DB 17; Length 1 Similarity 73.9%; Pred. No. 3.88+05; 34; Conservative 0; Mismatches 12; Indels
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Tel: 81-298-53-4664
Fax: 81-298-53-6614
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Pred. No. 4e+05;
0; Mismatches 17;
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Location/Qualifiers
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/clone="VSH438"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
El (bases 1 to 66)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longaare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Waiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RM. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
                                                                                                                                                                                                                                                                                                                                                                                             electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicilin resistance."
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2M0017J07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0017J07 R, DNA sequence.
                                                                                                                      /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Insert Length: 10000 Std Error: 0.00
Plate: 0017 row: J column: 07
Seg primer: CACACAGGAAACAGCTATGACC
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/db_xref="taxon:10090"
                       /clone="UUGC2M0012N23"
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genet
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AZ780364/C
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(http://www.lax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gild/32114 gib/H23072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

(Dasas I to 58)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theisingy, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Washu Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B1846606 51 2ebrafish neuronal Danio rerio cDNA clone 4886602 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: zbrafish@watson.wustl.edu
ODNA Library constructed by S. Lin DNA Sequencing by: Washington
University Genome Sequencing Center Clone distribution: the
I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2789 AGACATATAAGGAAAATATTGAATTAAAAGAAAACGATGAAAAGGATGAAAGCAATGAAGA 2848
                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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/db_xref="taxon:10090"
/clone="UUGC2M0017J07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25.8; DB 17; Length 66; Pred. No. 6.6e+05; Mismatches 22; Indels
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 62)

I (bases 1 to 62)

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

I Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine

H444 Forset Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
                                                                                                                                                                                                                                            AI125009 62 bp mRNA linear EST 11-SEP-1998 ao13g09.s1 Barstead aorta HPLRB3 Homo sapiens cDNA clone IMAGE:1726528 3', mRNA sequence.
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603185478F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5258275 5',
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3'); double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCGGATCCAAC 3' and 5' GTTGGATCCG 3'], digested with Not I and cloned into the Not I and Eco RI sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 Fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the modified pT7T3 vector. Library constructed by Bob Barstead."
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                                                                                                   2789 AGACATATAAGGAAAATATTGAATTAAAAGAAAACGATGAAAAGATGAAAGCAATGAA 2846
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Pred. No. 7.8e+05;
Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Barstead aorta HPLRB3"
0.3%; Scor
63.8%; Pred. No. /...
1; Mismatches
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/dev_stage="adult, age 64"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1726528"
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                    Query Match
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AI125009/c
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JOURNAL
COMMENT
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                                                            Matches
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KEYWORDS
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LOCUS
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS02MCN 61 bp DNA linear GSS 14-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 149K23 of library G from Tetraodon nigroviridis, genomic survey
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Terraodontidae; Terraodon.

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Human gene number estimate provided by genome wide analysis using Tetraodon nigrouidis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 61)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                           /dev_stage="adult"
//lab_host="DH10B (phage-resistant)"
//note="Organ: brain; Vector: pBluescript (modified);
Site_1: DraIII(Y); Site_2: DRAIII(X); Library is cloned
directionally between the DraIII(X) and DraIII(Y) sites
and has been amplified. Library constructed by S. Lin. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Genoscope sequence ID : COAG149AF12SP1~end
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                                                                                                                                                                                                                                                                                                                                                            0.3%; Score 25.6; DB 13; Length 58; 70.8%; Pred. No. 7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1047 ACAATATTCACAGCAACAAAATTCTCCACAAAAACATAAGAACAAAGA 1094
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                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
                                                                                                /clone="4886602"
/clone_lib="Zebrafish neuronal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                        /organism="Danio rerio"
/db_xref="taxon:7955"
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence. Tetraodon nigroviridis.
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                                                                                                                                           /sex-"mixed"
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 70.8
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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ORIGIN
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CNS02MCN/c
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Matches 39; Conservative
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Fax: 801 585 7177
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/db_xref="taxon:9666"
/db_xref="Iaxon:9666"
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/clone="Iaxon:9666"
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/tasue_type="epithelioid carcinoma cell line"
/tasue_type="epithelioid" carcinoma 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63) .
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Onpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lll.gov
http://image.lll.gov
lighte: LLCM1869 row: 1 column: 20
High quality sequence stop: 63.
Location/Qualifiers
                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
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BI457211
BI457211.1 GI:15247867
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A2375608 100129M04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0129M04 F, DNA sequence.
                                  Sequencing Center
information can be
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//note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 59)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aoyagi, A., Barber, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9307 CAGCAAATAACTGAGGTCTTTGTATTAGCAGAAGAATAGAAATAAACAGAAATGAAAAG 9366
                                                                                                                                                                                                                  1. .66
/orgatism="Homo sapiens"
/orgatism="taxon:9606"
/clone="IMAGE:2436117"
/clone=lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, pooled tumors"
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CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-lbio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco.
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62.9%; Pred. No. 8.7e+05;
tive 0; Mismatches 23;
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Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: M column: 04
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Class: plasmid ends
High quality sequence stop: 59.
Location/Qualifiers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Lin Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA215584.1 GI:1815420
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Best Local Similarity 69.4%;
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                                                                                                                                                                           ORIGIN
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                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gild732114)gblAEL3072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 21-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 61)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
                                                                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602145034F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4308440 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 0.3%; Score 25; DB 17; Length 59; Similarity 75.6%; Pred. No. 9.2e+05; 31; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1180 row: d column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9329 TATTAGCAGAAAGAATAGAAATAAACAGAAATGAAAAGAAG 9369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:4308440"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 61.
  /clone="UUGC1M0129M04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF663117.1 GI:11937012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BF663117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF663117
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                    EST 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 66)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4Iml3 fwd. ET from Amersham
High quality sequence stop: 50.
Location/Qualifiers
                                                                                                                                                                                                                    AA215584 66 bp mRNA linear EST 13-AUG-1 zr96c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683530 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2801 AAAATATTGAATTAAAAGAAAACGATGAAAAGATGAAAGCAATGAAGAGGATCAAGAACTT 2860
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                        4470 CAAAATAGCCTGCAGATCACAACCAGACCCAGTGGACACACCAACAAGC 4518
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Length 61;
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Pred. No. 1e+06;
0; Mismatches 22; Indels
                                                                                               15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:683530"
/clone_11b="NCI_GGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
Score 25; DB 12;
Pred. No. 9.3e+05;
                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GDB:5586850"
/db_xref="taxon:9606"
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